

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:15:56 ; Search time 44 Seconds
(Without alignments)
43.697 Million cell updates/sec

Title: US-09-651-685a-5

Sequence: 1 CCYDGSVNNDETCEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: PIR73:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	95.6	1676	1 C5HU	complement C5 prec
2	94	82.5	74	2 A25408	complement C5 - bo
3	93	81.6	74	2 A01268	complement C5 - p1
4	84	73.7	77	2 A57689	complement C5a - r
5	84	73.7	1680	1 C5MS	complement C5 prec
6	56.5	49.6	1735	2 S54784	sex-limited protel
7	56.5	49.6	1736	2 A29176	sex-limited protel
8	56.5	49.6	1738	1 A24558	complement C4 prec
9	55.5	48.7	76	2 J10036	complement C4a ana
10	55.5	48.7	77	2 A01265	complement C4 - bo
11	51.5	45.2	1744	1 C4HU	complement C4a pre
12	48	42.1	135	2 D44503	p19 protein - beet
13	48	42.1	282	2 JC5677	RNA4 protein - beet
14	48	42.1	282	2 C44503	P31 protein - beet
15	47	40.2	834	2 J01965	hypothetical 94K p
16	46	40.4	1473	2 A20872	ovostatin precursor
17	45.5	39.9	1617	2 T28153	complement C4 - ch
18	45	39.5	159	2 E66760	conserved hypotet
19	45	39.5	394	2 T21013	hypothetical prote
20	44.5	39.0	161	2 S44619	C50C3.9 protein -
21	44.5	39.0	281	2 S73895	hypothetical prote
22	44.5	39.0	669	2 S65551	factor H - bovine
23	44	38.6	68	2 AE3441	17K common-antigen
24	44	38.6	2095	2 S29529	genome polypeptide
25	43.5	38.2	241	2 A58262	telraspan TSPAN-1
26	43.5	38.2	1651	1 C3NU	complement C3 prec
27	43	37.7	198	2 H90111	26S proteasome, be
28	43	37.7	337	2 T18654	hypothetical prote
29	43	37.7	461	2 AH0373	cysteine-tRNA 11ga

30	43	37.7	1645	2 AG1897	two-component hybr
31	43	37.7	2543	2 T31687	surface antigen - p
32	42.5	37.3	685	2 S78040	fibulin, splice fo
33	42.5	37.3	705	2 S34968	fibulin, splice fo
34	42.5	37.3	1620	2 S15339	complement compone
35	42.5	37.3	1673	2 T50806	complement compone
36	42	36.8	368	2 H75412	spermidine/putresc
37	42	36.8	1068	2 S01519	genome polypeptide
38	42	36.8	2092	2 S30026	hypothetical prote
39	42	36.8	2149	2 S18676	hypothetical prote
40	41.5	36.4	312	2 T32379	hypothetical prote
41	41.5	36.4	616	2 T32379	hypothetical prote
42	41.5	36.4	1101	2 T16840	hypothetical prote
43	41	36.0	187	2 T48093	hypothetical prote
44	41	36.0	208	2 C96833	hypothetical prote
45	41	36.0	217	2 A87990	protein W05H12.1 l

ALIGNMENTS

RESULT 1
C5HU
complement C5 precursor [validated] - human
N:Contains: C5a anaphylatoxin; C5b
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text_change 08-Dec-2000
C:Accession: A40075; A27689; A01267; A01266; S15121
R:Haviland, D.L.; Haviland, J.C.; Fleischner, D.T.; Hunt, A.; Wetsel, R.A.
J. Immunol. 146, 362-368, 1991
A:Title: Complete cDNA sequence of human complement pro-C5. Evidence of truncated tra
A:Reference number: A40075; MUID:91079575; PMID:1984448
A:Accession: A40075
A:Molecule type: mRNA
A:Residues: 1-1676 <HAV>
A:Cross-references: GB:M57729; NID:g179982; PIDN:AAA51925.1; PID:g179983
A:Note: S18-Ser was also found
R:Wetsel, R.A.; Lemons, R.S.; Le Beau, M.M.; Barnum, S.R.; Noack, D.; Tack, B.F.
Biochemistry 27, 1474-1482, 1988
A:Title: Molecular analysis of human complement component C5: localization of the str
A:Reference number: A27689; MUID:88209511; PMID:3365401
A:Accession: A27689
A:Molecule type: mRNA
A:Residues: 412-1676 <MBT>
A:Cross-references: GB:M65134; GB:M18879; NID:g179691; PIDN:AAA51856.1; PID:g179692
R:Fernandez, H.N.; Hugli, T.E.
J. Biol. Chem. 263, 6955-6964, 1978
A:Title: Primary structural analysis of the polypeptide portion of human C5a anaphyla
A:Reference number: A01267; MUID:79005687; PMID:690134
A:Accession: A01267
A:Molecule type: protein
A:Residues: 678-751 <FER>
R:Lundvall, A.B.; Wetsel, R.A.; Kristensen, T.; Whitehead, A.S.; Woods, D.E.; Ogden,
J. Biol. Chem. 260, 2108-2112, 1985
A:Title: Isolation and sequence analysis of a cDNA clone encoding the fifth complemen
A:Reference number: A01266; MUID:85130937; PMID:2579066
A:Accession: A01266
A:Molecule type: mRNA
A:Residues: 412-854, 'STALSRLCNGKISGCKLRLPSSDSFASASQVAGITGTHHHAQT' <LUN>
A:Cross-references: GB:K02874
A:Note: The carboxyl-terminal part of the sequence in this report appears to be deriv
R:Bohnsack, J.F.; Mollison, K.W.; Buko, A.M.; Ashworth, J.C.; Hill, H.R.
Biochem. J. 273, 635-640, 1991
A:Title: Group B streptococci inactivate complement component C5a by enzymic cleavage
A:Reference number: S15121; MUID:91144547; PMID:1996561
A:Contents: annotation
C:Comment: Complement C5 contains two disulfide-linked chains, formed by removal of f
(beta and alpha' chains').
C:Comment: Activation of C5 initiates the spontaneous assembly of the late complement
is the foundation upon which the membrane attack complex is assembled.
C:Comment: C5a has potent spasmogenic and chemotactic activity.
C:Genetics:
A:Gene: GDB:C5

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Proc. Natl. Acad. Sci. U.S.A. 78, 1833-1837, 1981
A:Reference number: A26247; MUID:81199549; PMID:6940191
A:Contents: annotation; active region
A>Note: although Arg-74 is not essential, residues 72-74 (Leu-Gly-Arg) are required for
R.Zimmermann, B.; Vogt, W.
Hoppe-Seyler's Z. Physiol. Chem. 365, 151-158, 1984
A:Reference number: A26248; MUID:84184201; PMID:6714942
A:Contents: disulfide bonds
A:Accession: A26248
A:Molecule type: protein
A:Residues: 1-64, E',66-73 <ZIM>
C:Comment: Complement C5 contains two disulfide-linked chains, formed by removal of f
(beta and alpha' chains).
C:Comment: Activation of C5 initiates the spontaneous assembly of the late complement
is the foundation upon which the membrane attack complex is assembled.
C:Comment: C5a has potent spasmogenic and chemotactic activity.
C:Superfamily: alpha-2-macroglobulin
C:Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein
F:1-47/22-54,34-55/Disulfide bonds #status experimental
F:21-47,22-54,34-55/Disulfide bonds #status experimental

Query Match      81.6%; Score 93; DB 2; Length 74;
Best Local Similarity 80.0%; Pred. No. 2.4e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY      1 CCYDGASVNNDETCEORAR 20
        |||||  |||||:||||
Db      21 CCYDGAVRNDETCEERAR 40

RESULT 4
A57689
complement C5a - rat (fragment)
N:Contains: C5a anaphylatoxin; C5b
C:Species: Rattus norvegicus (Norway rat)
C>Date: 23-Feb-1996 #sequence_revision 31-Jan-1997 #text_change 16-Feb-1997
C:Accession: A57689
R:Cui, L.; Carney, D.F.; Hugli, T.E.
Protein Sci. 3, 1169-1177, 1994
A:title: Primary structure and functional characterization of rat C5a: an anaphylatox
A:Reference number: A57689; MUID:95078724; PMID:7987212
A:Accession: A57689
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-77 <CUI>
C:Complex: Complement C5 contains two disulfide-linked chains, formed by removal of f
(beta and alpha' chains).
C:Function:
A:Description: activation of C5 initiates spontaneous assembly of the late complement
is the foundation for assembly of the membrane attack complex
A:Pathway: complement alternate pathway; complement pathway
A>Note: C5a has potent spasmogenic and chemotactic activity
C:Superfamily: alpha-2-macroglobulin
C:Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein
F:1-77/Product: C5a anaphylatoxin #status experimental <C5T>
F:24-50,25-57,37-58/Disulfide bonds #status predicted

Query Match      73.7%; Score 84; DB 2; Length 77;
Best Local Similarity 75.0%; Pred. No. 6.1e-06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY      1 CCYDGASVNNDETCEORAR 20
        |||||  |||||:||||
Db      24 CCYDGARENKJETCEORAR 43

RESULT 5
C5MS
complement C5 precursor - mouse
N:Contains: C5a anaphylatoxin; C5b
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988#sequence_revision 15-Oct-1994 #text_change 18-Jun-1999

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R:Wetzel, R.A.; Fleischer, D.T.; Haviland, D.L.
 J. Biol. Chem. 265, 2435-2440, 1990
 A:Title: Deficiency of the murine fifth complement component (C5). A 2-base pair gene deletion.
 A:Reference number: A35530; MUID:90153853; PMID:2303408
 A:Accession: A35530
 A:Molecule type: mRNA
 A:Residues: 1-215, 'L' <RES>
 A:Cross-references: GB:M5526; GB:J05234; NID:g192302; PIDN:AAA37348.1; PID:g309123
 R:Wetzel, R.A.; Ogata, R.T.; Tack, B.F.
 Biochemistry 26, 737-743, 1987
 A:Title: Primary structure of the fifth component of murine complement.
 A:Reference number: A27538; MUID:87185363; PMID:2436653
 A:Accession: A27538
 A:Molecule type: mRNA
 A:Residues: 'PGL', 44-1680 <MET2>
 R:Haviland, D.L.; Fleischer, D.T.; Wetzel, R.A.
 J. Biol. Chem. 266, 11818-11825, 1991
 A:Title: Structure of the murine fifth complement component (C5) gene. A large, highly intact component genes.
 A:Reference number: A40429; MUID:91268053; PMID:1711041
 A:Accession: A40429
 A:Molecule type: DNA
 A:Residues: 1-15 <HAV>
 A:Cross-references: GB:M64852
 C:Comment: Complement C5 contains two disulfide-linked chains, formed by removal of four (beta and alpha chains).
 C:Comment: Activation of C5 initiates the spontaneous assembly of the late complement cascade, the foundation upon which the membrane attack complex is assembled.
 C:Comment: C5a has potent spasmogenic and chemotactic activity.
 C:Genetics:
 A:Map position: 2
 A:Introns: 22/3; 86/3; 140/3; 164/3; 195/2; 223/1; 253/2; 291/3; 334/1; 372/3; 434/3; 503; 1224/1; 1292/3; 1343/3; 1364/3; 1392/1; 1411/2; 1445/3; 1470/3; 1506/1; 1534/1; 1564/3; Superfamily: alpha-2-macroglobulin
 C:Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; I
 F:1-18/Domain: signal sequence #status predicted <STG>
 F:19-674, 679-1679/Product: complement C5 #status predicted <C5B>
 F:19-674, 756-1679/Product: complement C5 #status predicted <C5B>
 F:19-674/Product: complement C5 and C5b beta chain #status predicted <C5BB>
 F:679-1679/Product: complement C5 alpha chain #status predicted <C5A>
 F:679-755/Product: C5a anaphylatoxin #status predicted <C5T>
 F:756-1679/Product: C5b alpha' chain #status predicted <C5BA>
 F:567-814, 635-670, 702-728, 703-735, 715-736, 870-1531, 1105-1163, 1379-1509, 1403-1478, 1524-1591, 915, 1119, 1633/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.7% Score 84; DB 1; Length 1680;
 Best Local Similarity 75.0% Pred. No. 0.00011;
 Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCYGCASVNDTCGEORAR 20
 ||||| || ||||| ||
 Db 702 CCYGCARVNFETCEERVAR 721

RESULT 6
 S54784
 sex-limited protein Slp(w7) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
 C:Accession: S54784; MUID:148770
 R:Ogata, R.T.; Zepf, N.E.
 J. Immunol. 147, 2756-2763, 1991
 A:Title: The murine Slp gene. Additional evidence that sex-limited protein has no biologic function.
 A:Reference number: S54784; MUID:92013090; PMID:1918990
 A:Accession: S54784
 A:Molecule type: DNA
 A:Status: preliminary; translation not shown
 A:Residues: 1-1735 <OGA>
 A:Cross-references: EMBL:M6933; NID:g200988; PIDN:AAA40117.1; PID:g200989
 R:Hemmenway, C.; Kalif, M.; Stavenhagen, J.; Walhall, D.; Robins, D.
 Nucleic Acids Res. 14, 2539-2554, 1986
 A:Title: Sequence comparison of alleles of the fourth component of complement (C4) and S

A:Accession: 148770
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 634-641, 'L', 643-828 <RES>
 A:Cross-references: EMBL:X06455; NID:g54102; PIDN:CAA29761.1; PID:g899336
 C:Genetics:
 A:Introns: 22/2; 86/3; 154/1; 177/3; 207/2; 235/1; 267/2; 302/3; 347/1; 385/3; 444/3; 3; 1219/1; 1296/3; 1352/3; 1372/3; 1404/1; 1464/2; 1494/3; 1519/3; 1554/1; 1584/1; 16
 C:Superfamily: alpha-2-macroglobulin

Query Match 49.6% Score 56.5; DB 2; Length 1735;
 Best Local Similarity 57.1% Pred. No. 2;
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 CCYDCASVNDTCGEORAR 20
 ||||| || ||||| ||
 Db 700 CCQDCGTRKPMKRTCEORAR 720

RESULT 7
 A29176
 sex-limited protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
 C:Accession: A29176; B21692; A41195; B29059; B60227; I79467
 R:Ogata, R.T.; Sepich, D.S.
 J. Immunol. 135, 4239-4244, 1985
 A:Title: Murine sex-limited protein: complete cDNA sequence and comparison with murin
 A:Reference number: A29176; MUID:86060918; PMID:3840826
 A:Accession: A29176
 A:Molecule type: mRNA
 A:Residues: 1-1736 <OGA>
 R:Nonaka, M.; Takahashi, M.; Natsume-Sakai, S.; Nonaka, M.; Tanaka, S.; Shimizu, A.;
 Proc. Natl. Acad. Sci. U.S.A. 81, 6822-6826, 1984
 A:Title: Isolation of cDNA clones specifying the fourth component of mouse complement
 A:Reference number: A94013; MUID:85038607; PMID:6208559
 A:Accession: B21692
 A:Molecule type: mRNA
 A:Residues: 651-749, 'H', 751-774, 'D', 776-802, 921-1040 <NON>
 R:Ogata, R.T.; Sepich, D.S.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4908-4911, 1984
 A:Title: Genes for murine fourth complement component (C4) and sex-limited protein (S
 A:Reference number: A41195; MUID:84272739; PMID:6589636
 A:Accession: A41195
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1345-1438, 'R', 1440-1544 <OG2>
 A:Cross-references: GB:K02293; NID:g199611; PIDN:AAA39682.1; PID:g199612
 R:Tosi, M.; Levi-Strauss, M.; Duponchel, C.; Meo, T.
 Philos. Trans. R. Soc. Lond. 306, 389-394, 1984
 A:Title: Sequence heterogeneity of murine complementary DNA clones related to the C4
 A:Reference number: A93753
 A:Accession: B29059
 A:Molecule type: mRNA
 A:Residues: 1255-1335, 'G', 1337-1373 <TOS>
 R:Ogata, R.T.; Zepf, N.E.
 Eur. J. Immunol. 20, 1607-1610, 1990
 A:Title: C4 from C4-high and C4-low mouse strains have identical sequences in the reg
 A:Reference number: A60227; MUID:90353398; PMID:2387317
 A:Accession: B60227
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1096-1139 <OG3>
 A:Cross-references: GB:X55495
 R:Nonaka, M.; Kimura, H.; Teul, Y.D.; Yokoyama, S.; Nakayama, K.; Takahashi, M.
 Proc. Natl. Acad. Sci. U.S.A. 83, 7883-7887, 1986
 A:Title: Identification of the 5'-flanking regulatory region responsible for the diff
 A:Reference number: I59084; MUID:87017050; PMID:3464002
 A:Accession: I79467
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-21 <RES>

A:Cross-references: GB:M14225; NID:g199615; PIDN:AAA39684.1; PID:g554239
 C:Genetics:
 A:Gene: s1p
 C:Superfamily: alpha-2-macroglobulin
 F:1-19/Domain: signal sequence #status predicted <Sts>
 F:20-1736/Product: sex-limited protein #status predicted <MAt>

Query Match 49.6%; Score 56.5; DB 2; Length 1736;
 Best Local Similarity 57.1%; Pred. No. 2;
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;
 Oy 1 CCYGS-ASVNDTECEORAR 20-
 |||||
 Db 700 CCODGMRKLPKMRCEORAR 720

RESULT 8

A24558
 Complement C4 precursor - mouse
 N/Contains: classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) C4b subunit; co
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Mar-1989 #sequence revision 11-Nov-1994 #text-change 18-Jun-1999
 C/Accession: A24558; A25371; A21692; A30520; A60227; A22039; A29059; A01264; B41195; I59
 R:Sepich, D.S.; Noonan, D.J.; Ogata, R.T.
 Proc. Natl. Acad. Sci. U.S.A. 82, 5895-5899, 1985
 A:Title: Complete cDNA sequence of the fourth component of murine complement.
 A:Reference number: A24558; MUID:85298264; PMID:3862104
 A:Accession: A24558
 A:Molecule type: mRNA
 A:Residues: 1-1738 <SEP>
 A:Cross-references: GB:M11729; NID:g199080; PIDN:AAA39506.1; PID:g387420
 A:Experimental source: strain B10.WR
 R:Nonaka, M.; Nakayama, K.; Yeul, Y.D.; Takahashi, M.
 J. Biol. Chem. 260, 10936-10943, 1985
 A:Title: Complete nucleotide and derived amino acid sequences of the fourth component of
 A:Reference number: A25371; MUID:85289294; PMID:2993295
 A:Accession: A25371
 A:Molecule type: mRNA
 A:Residues: 1-131; 'Y', '133-326', 'E', '328-569', 'E', '571-1323', 'N', '1325-1441', 'K', '1443-1452', 'V', '1
 A:Cross-references: GB:M11789
 A:Experimental source: strain FM
 R:Nonaka, M.; Takahashi, M.; Natsunume-Sakai, S.; Nonaka, M.; Tanaka, S.; Shimizu, A.; Ho
 Proc. Natl. Acad. Sci. U.S.A. 81, 6822-6826, 1984
 A:Title: Isolation of cDNA clones specifying the fourth component of mouse complement an
 A:Reference number: A94013; MUID:85038607; PMID:6208559
 A:Accession: A21692
 A:Molecule type: mRNA
 A:Residues: 651-719; 'G', '721-738', 'A', '741-805 <NO2>
 A:Cross-references: GB:M12970
 A:Experimental source: strain FM
 R:Tallion-Miller, P.A.; Shreffler, D.C.
 J. Immunol. 141, 2382-2387, 1988
 A:Title: Structural basis for the C4d.1/C4d.2 serologic allotypes of murine complement c
 A:Reference number: A30520; MUID:89009745; PMID:2459207
 A:Accession: A30520
 A:Molecule type: DNA
 A:Residues: 961-1205; 'Q', '1207-1290 <TAI>
 A:Cross-references: GB:M23186; NID:g340821; PIDN:AAA40487.1; PID:g554392
 A:Experimental source: strain B10.BR
 R:Ogata, R.T.; Zepf, N.E.
 Eur. J. Immunol. 20, 1607-1610, 1990
 A:Title: C4 from C4-high and C4-low mouse strains have identical sequences in the region
 A:Reference number: A60227; MUID:90353398; PMID:2387317
 A:Accession: A60227
 A:Molecule type: DNA
 A:Residues: 1099-1142 <OGA>
 A:Cross-references: GB:555433; NID:g287729; PIDN:CAA39112.1; PID:g287730
 R:Levi-Strauss, M.; Tosi, U.S.A. 82, 1746-1750, 1985
 Proc. Natl. Acad. Sci. U.S.A. 82, 1746-1750, 1985
 A:Title: Multiple duplications of the complement C4 gene correlate with H-2-controlled test
 A:Reference number: A22039; MUID:85166208; PMID:3856857
 A:Accession: A22039
 A:Molecule type: mRNA

A:Residues: 1105-1118; 'A', '1120-1189', 'T', '1191-1449 <LEV>
 A:Cross-references: GB:K02798; NID:g199281; PIDN:AA42021.1; PID:g199282
 A:Experimental source: strain B10.W7R
 R:Tosi, M.; Levi-Strauss, M.; Duponchel, C.; Meo, T.
 Philos. Trans. R. Soc. Lond. 306, 389-394, 1984
 A:Title: Sequence heterogeneity of murine complementary DNA clones related to the C4
 A:Reference number: A93753
 A:Accession: A29059
 A:Molecule type: mRNA
 A:Residues: 1258-1376 <TOS>
 A:Cross-references: GB:K02798
 R:Ogata, R.T.; Shreffler, D.C.; Sepich, D.S.; Lilly, S.P.
 Proc. Natl. Acad. Sci. U.S.A. 80, 5061-5065, 1983
 A:Title: cDNA clone spanning the alpha-gamma subunit junction in the precursor of the
 A:Reference number: A01264; MUID:83273751; PMID:6192448
 A:Accession: A01264
 A:Molecule type: mRNA
 A:Residues: 1360-1400; 'S', '1402-1511 <OG2>
 A:Cross-references: GB:K00019; NID:g199259; PIDN:AAA39554.1; PID:g554209
 A:Experimental source: strain B10.W7R
 R:Ogata, R.T.; Sepich, D.S.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4908-4911, 1984
 A:Title: Genes for murine fourth complement component (C4) and sex-limited protein (S
 A:Reference number: A41195; MUID:84272739; PMID:6589636
 A:Accession: B41195
 A:Molecule type: mRNA
 A:Residues: 1360-1400; 'S', '1402-1511 <OG3>
 A:Cross-references: GB:K00019; NID:g199259; PIDN:AAA39554.1; PID:g554209
 A:Experimental source: strain B10.W7R
 R:Nonaka, M.; Kimura, H.; Yeul, Y.D.; Yokoyama, S.; Nakayama, K.; Takahashi, M.
 Proc. Natl. Acad. Sci. U.S.A. 83, 7883-7887, 1986
 A:Title: Identification of the 5'-flanking regulatory region responsible for the diff
 A:Reference number: 159084; MUID:87017050; PMID:3464002
 A:Accession: 159084
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-21 <RES>
 A:Cross-references: GB:M14225; NID:g199291; PIDN:AAA39563.1; PID:g554211
 R:Hemenway, C.; Kalf, M.; Steinhagen, J.; Walthall, D.; Robins, D.
 Nucleic Acids Res. 14, 2539-2554, 1986
 A:Title: Sequence comparison of alleles of the fourth component of complement (C4) an
 A:Reference number: 148274; MUID:86176748; PMID:3008092
 A:Accession: 148274
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 591-603; 'M', '605-1323', 'N', '1325-1452', 'V', '1454-1585', 'Q', '1587-1738 <RE2>
 A:Cross-references: EMBL:X05314; NID:g50241; PIDN:CAA28936.1; PID:g50242
 R:Nonaka, M.; Nakayama, K.; Yeul, Y.D.; Shimizu, A.; Takahashi, M.
 Immunol. Rev. 87, 81-99, 1985
 A:Title: Molecular cloning and characterization of complementary and genomic DNA clon
 A:Reference number: 154567; MUID:86031969; PMID:2997024
 A:Accession: 154567
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-128 <RE3>
 A:Cross-references: GB:M12968; NID:g199267; PIDN:AAA39558.1; PID:g199270
 A:Accession: 169023
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1724-1738 <RE4>
 A:Cross-references: GB:M12969; NID:g199268; PIDN:AAA39559.1; PID:g387439
 C/Comment: This protein is synthesized as a single-chain precursor and, prior to secr
 by disulfide bonds.
 C/Comment: The activation of complement C4 by complement subcomponent C1s releases th
 of complement factor 2 to form the classical-complement-pathway C3 convertase. The C
 ay C5 convertase.
 C/Comment: C4a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
 C/Comment: The activity of C4b is regulated by proteolytic cleavage involving C4b-Bin
 C:Genetics:
 A:Introns: 22/2; 86/3; 97/3; 104/3; 107/3; 1125/3; 1164/3; 1221/3
 A:Note: The list of introns is incomplete
 C:Superfamily: alpha-2-macroglobulin
 C:Keywords: acute phase; complement classical pathway; glycoprotein; hydrolase; infla

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-673/Product: complement C4 beta chain #status predicted <BET>
F:20-673/54-1440,1448-1738/Product: complement C4b #status predicted <C4b>
F:678-1440/Product: complement C4 alpha chain #status predicted <ALP>
F:678-753/Product: C4a anaphylatoxin #status predicted <C4a>
F:754-443/Region: C4b-binding protein binding
F:953-1332/Product: C4d fragment #status predicted <C4d>
F:1448-1738/Product: complement C4 gamma chain #status predicted <GAM>
F:224/743,1387/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:753-754/Cleavage site: Arg-Asn (complement subcomponent C1s) #status predicted
F:1006-1009/Cross-link: thiolester (Cys-Gln) #status predicted

Query Match 49.6%; Score 56.5; DB 1; Length 1738;
Best Local Similarity 57.1%; Pred. No. 2;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

OY 1 CCYDG-ASVNDTECEQRAAR 20
||| : |||||
Db 700 CCODGMRKLPKRTCEQRAAR 720

RESULT 9

JL0036
complement C4a anaphylatoxin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 15-Nov-1996
C:Accession: JL0036
R:Cul, L.; Ferreri, K.; Hugli, T.E.
Mol. Immunol. 25, 663-671, 1988
A:Title: Structural characterization of the C4a anaphylatoxin from rat.
A:Reference number: JL0036; MUID:88334568; PMID:3262196
A:Accession: JL0036

A:Molecule type: protein
A:Residues: 1-76 <CU1>
C:Superfamily: alpha-2-macroglobulin
C:Keywords: complement classical pathway; glycoprotein
F:66/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 48.7%; Score 55.5; DB 2; Length 76;
Best Local Similarity 57.1%; Pred. No. 0.15;

Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

OY 1 CCYDG-ASVNDTECEQRAAR 20
||| : |||||
Db 23 CCODGMRKLPKRTCEQRAAR 43

RESULT 10

A01265
complement C4 - bovine (fragment)
N:Contains: C4a anaphylatoxin; classical-complement-pathway C3/C5 convertase (EC 3.4.21.1)
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jun-1983 #sequence_revision 15-Oct-1994 #text_change 16-Feb-1997
C:Accession: A01265
R:Smith, M.A.; Gerrie, L.M.; Dunbar, B.; Fothergill, J.E.
Biochem. J. 207, 253-260, 1982
A:Title: Primary structure of bovine complement activation fragment C4a, the third anaphylatoxin
A:Reference number: A01265; MUID:83126436; PMID:6760852
A:Accession: A01265

A:Molecule type: protein
A:Residues: 1-77 <SM1>
C:Superfamily: alpha-2-macroglobulin
C:Keywords: complement pathway; glycoprotein; hydrolase; inflammation; plasma; serine protease
F:1-77/Product: C4a anaphylatoxin #status experimental <C4a>

Query Match 48.7%; Score 55.5; DB 2; Length 77;
Best Local Similarity 57.1%; Pred. No. 0.15;

Matches 12; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

OY 1 CCYDG-ASVNDTECEQRAAR 20
||| : |||||
Db 23 CCODGMRKLPKRTCEQRAAR 43

RESULT 11

C4HU

complement C4a precursor [validated] - human

N:Contains: classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) C4b subunit;
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1985 #sequence_revision 23-Aug-1996 #text_change 08-Dec-2000
C:Accession: I56095; A29177; B29177; A90845; A19311; A92337; S12866; A17265; A32335;
R:Yu, C.Y.
J. Immunol. 146, 1057-1066, 1991

A:Title: The complete exon-intron structure of a human complement component C4a gene.
A:Reference number: I56095; MUID:91108039; PMID:1988494
A:Accession: I56095

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1744 <RES>

A:Cross-references: GB:M59815; NID:g179672; PIDN:AAA51855.1; PID:g179674

R:Belt, K.T.; Yu, C.Y.; Carroll, M.C.; Porter, R.R.
Immunogenetics 21, 173-180, 1985

A:Title: Polymorphism of human complement component C4.
A:Reference number: A29177; MUID:85156269; PMID:3838531

A:Accession: A29177

A:Molecule type: DNA

A:Residues: 1056-1225 <BE3>

A:Cross-references: GB:M14824; NID:g179675; PIDN:AAA52292.1; PID:g553210

R:Belt, K.T.; Carroll, M.C.; Porter, R.R.
Cell 36, 907-914, 1984

A:Title: The structural basis of the multiple forms of human complement component C4.
A:Reference number: A90845; MUID:84156544; PMID:6546707

A:Accession: A90845

A:Molecule type: mRNA

A:Residues: 20-346, 'S', 348-417, 'A', 419-725, 'P', 727-1200, 'S', 1202-1285, 'S', 1287-1418, 1

A:Cross-references: GB:R02403

R:Carroll, M.C.; Porter, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 264-267, 1983

A:Title: Cloning of a human complement component C4 gene.
A:Reference number: A19311; MUID:83117835; PMID:6572000

A:Accession: A19311

A:Molecule type: mRNA

A:Residues: 1195-1285, 'S', 1287-1294 <CAR>

A:Cross-references: GB:J00080; NID:g30010; PIDN:CAA23760.1; PID:g1335030

R:Moyn, K.E.; Gorski, J.P.; Hugli, T.E.
J. Biol. Chem. 256, 8685-8692, 1981

A:Title: Complete primary structure of human C4a anaphylatoxin.
A:Reference number: A92337; MUID:81264286; PMID:6167582

A:Accession: A92337

A:Molecule type: protein

A:Residues: 680-725, 'PN', 728-756 <MOO>

R:Hessing, M.; van't Veer, C.; Hackeng, T.M.; Bouma, B.N.; Iwanaga, S.
FEBS Lett. 271, 131-136, 1990

A:Title: Importance of the alpha(3)-fragment of complement C4 for the binding with C4
A:Reference number: S12866; MUID:91032049; PMID:1699796

A:Accession: S12866

A:Molecule type: protein

A:Residues: 757, 'X', 759-771, 980-990 <HES>

R:Campbell, R.D.; Gagnon, J.; Porter, R.R.
Biochem. J. 199, 359-370, 1981

A:Title: Amino acid sequence around the thiol and reactive acyl groups of human compl
A:Reference number: A17265; MUID:82182029; PMID:6978711

A:Accession: A17265

A:Molecule type: protein

A:Residues: 957-1012, 'E', 1014-1108, 'I', 1110-1175, 'S', 1177-1270, 'V', 1272-1336 <CHA>

C:Accession: J01965
R:Takahashi, M.; Toriyama, S.; Hamamatsu, C.; Ishihama, A.
J. Gen. Virol. 74, 769-773, 1993
A:Title: Nucleotide sequence and possible ambisense coding strategy of rice stripe virus
A:Reference number: J01964, MUID:93224901, PMID:8468559
A:Accession: J01965
A:Molecule type: genomic RNA
A:Residues: 1-834 <TRK>
A:Cross-references: DDBJ:DJ1176; NID:9536885; PIDN:BAA02470.1; PID:91199491
C:Superfamily: rice stripe virus hypothetical 94K protein

Query Match 41.28; Score 47; DB 2; Length 834;
Best Local Similarity 69.28; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 CYDGASYNDETC 14
||:|||||
Db 69 CYNRASVNFETC 81

Search completed: May 1, 2003, 22:20:06
Job time : 46 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:09:31 : Search time 11 Seconds
(without alignments)
75.412 Million cell updates/sec

Title: US-09-651-685a-5
Perfect score: 114
Sequence: 1 CCYDGSVNNDETCEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	95.6	1676	1 CO5_HUMAN	P01031 homo sapien
2	94	82.5	74	1 CO5A_BOVIN	P12082 bos taurus
3	93	81.6	74	1 CO5A_PIG	P01032 sus scrofa
4	84	73.7	76	1 CO5A_RAT	P08650 ratius norv
5	84	73.7	1680	1 CO5_MOUSE	P06684 mus musculu
6	56.5	49.6	1738	1 CO4_MOUSE	P01029 mus musculu
7	55.5	48.7	76	1 CO4A_RAT	P08649 ratius norv
8	55.5	48.7	920	1 CO4_BOVIN	P01030 bos taurus
9	51.5	45.2	1744	1 CO4_HUMAN	P01028 homo sapien
10	48	42.1	282	1 Y32K_BNYG	P19231 beet necrot
11	46	40.4	1473	1 OVOS_CHICK	P20740 gallus gall
12	44.5	39.0	281	1 Y125_MCPN	P75511 mycoplasma
13	44.5	39.0	685	1 CFAM_BOVIN	Q28085 bos taurus
14	44.5	39.0	1205	1 YLJ9_CAEEL	P24372 caenorhabdi
15	44	38.6	715	1 S141_HUMAN	Q92503 homo sapien
16	44	38.6	2095	1 RRP_L_TOSV	P27800 toscana vir
17	43.5	38.2	1651	1 CO3_NAJNA	Q01833 najia najia
18	43	37.7	337	1 DNJ2_GAEEL	Q02433 caenorhabdi
19	43	37.7	461	1 SYC_YERPE	Q82cc0 yersinia pe
20	42.5	37.3	705	1 FBLL_MOUSE	Q08879 mus musculu
21	42.5	37.3	1640	1 CO3_ONCMY	P88093 oncorhynch
22	42.5	37.3	1673	1 CO3_LAMJA	Q00685 lampetra ja
23	42	36.8	241	1 TSNI_HUMAN	Q06633 homo sapien
24	42	36.8	261	1 RFA4_HUMAN	Q13156 homo sapien
25	42	36.8	760	1 AD25_MOUSE	Q91159 mus musculu
26	42	36.8	1068	1 YCF0_MARPO	P12221 marcanthia
27	42	36.8	2149	1 RRP_L_RVPVZ	P27316 rift valley
28	41.5	36.4	65	1 MT_PARLI	P80367 paracentrol
29	41.5	36.4	486	1 MTR3_HUMAN	P18523 homo sapien
30	41	36.0	332	1 KZ2A_MAIZE	P28523 zea mays (m
31	41	36.0	450	1 YD10_BPTS	P11107 bacterioph
32	41	36.0	491	1 Y084_MCTU	O53209 mycobacteri
33	41	36.0	1826	1 SUI5_RABIT	P07766 oryctolagus

34	41	36.0	2230	1 GCG4_HUMAN	O13439 homo sapien
35	41	36.0	4543	1 LRP1_CHICK	P88157 gallus gall
36	41	36.0	4660	1 LRP2_RAT	P88158 ratius norv
37	40	35.1	351	1 Y4VJ_RHISN	Q53218 rhizobium s
38	40	35.1	366	1 YGDE_ECOLI	P32066 escherichia
39	40	35.1	448	1 EXG1_YEAST	P23776 saccharomyc
40	40	35.1	448	1 GRAN_DROME	P39572 drosophila
41	40	35.1	538	1 ADEC_MERTH	O26952 methanobact
42	40	35.1	581	1 PRIM_ECOLI	P02923 escherichia
43	40	35.1	581	1 PRIM_SALTY	P07362 salmonella
44	40	35.1	593	1 PRIM_HAEIN	O08346 haemophilus
45	40	35.1	813	1 AD33_HUMAN	Q9B211 homo sapien

ALIGNMENTS

RESULT 1	ID	CO5_HUMAN	STANDARD:	PRT: 1676 AA.
AC	P01031:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Complement C5 precursor [contains: C5a anaphylatoxin].			
CN	C5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Haviland D.L., Haviland J.C., Fleischer D.T., Hunt A., Wetsel R.A.;			
RT	"Complete cDNA sequence of human complement pro-C5. Evidence of			
RT	truncated transcripts derived from a single copy gene."			
RL	J. Immunol. 146:362-368(1991).			
RN	[2]			
RP	SEQUENCE OF 412-1676 FROM N.A.			
RX	MEDLINE=88209511; PubMed=3365401;			
RA	Wetsel R.A., Lemons R.S., Lebeau M.M., Barnum S.R., Noack D.,			
RA	Tack B.F.;			
RT	"Molecular analysis of human complement component C5: localization of			
RT	the structural gene to chromosome 9."			
RL	Biochemistry 27:1474-1482(1988).			
RN	[3]			
RP	SEQUENCE OF 412-902 FROM N.A.			
RX	MEDLINE=85130937; PubMed=2579066;			
RA	Lundwall A.B., Wetsel R.A., Kristensen T., Whitehead A.S.,			
RA	Woods D.E., Ogden R.C., Colten H.R., Tack B.F.;			
RT	"Isolation and sequence analysis of a cDNA clone encoding the fifth			
RT	complement component."			
RL	J. Biol. Chem. 260:2108-2112(1985).			
RN	[4]			
RP	SEQUENCE OF 678-751			
RX	MEDLINE=79005687; PubMed=690134;			
RA	Fernandez H.N., Hugli T.E.;			
RT	"Primary structural analysis of the polypeptide portion of human C5a			
RT	anaphylatoxin. Polypeptide sequence determination and assignment of			
RT	the oligosaccharide attachment site in C5a."			
RL	J. Biol. Chem. 253:6955-6964(1978).			
RN	[5]			
RP	SEQUENCE OF 678-751 FROM N.A.			
RX	MEDLINE=91144547; PubMed=1996961;			
RA	Bohnasack J.F., Mollison K.W., Buho A.M., Ashworth J.C., Hill H.R.;			
RT	"Group B streptococci inactivate complement component C5a by enzymic			
RT	cleavage at the C-terminus."			
RL	Biochem. J. 273:635-640(1991).			
RN	[6]			
RP	STRUCTURE BY NMR OF C5A.			
RX	MEDLINE=88309754; PubMed=3408713;			
RA	Zuidweg E.R.P., Mollison K.W., Henkin J., Carter G.W.;			
RT	"Sequence-specific assignments in the 1H NMR spectrum of the human			

RT inflammatory protein C5a.";
 RN Biochemistry 27:3568-3580(1988).
 [7]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE-89207527; PubMed-2784981;
 RA Zuideweg E.R.P., Nettesheim D.G., Mollison K.W., Carter G.W.;
 RT "tertiary structure of human complement component C5a in solution
 from nuclear magnetic resonance data.";
 RL Biochemistry 28:172-185(1989).
 [8]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE-89274164; PubMed-2730871;
 RA Zuideweg E.R.P., Fesik S.W.;
 RT "Heteronuclear three-dimensional NMR spectroscopy of the inflammatory
 protein C5a.";
 RL Biochemistry 28:2387-2391(1989).
 [9]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE-97160477; PubMed-9007977;
 RA Zhang X., Boyar W., Galakatos N., Gonnella N.C.;
 RT "Solution structure of a unique C5a semi-synthetic antagonist:
 implications in receptor binding.";
 RL Protein Sci. 6:65-72(1997).
 [10]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE-97332508; PubMed-9188742;
 RA Zhang X., Boyar W., Toth M.J., Mennog L., Gonnella N.C.;
 RT "Structural definition of the C5a C terminus by two-dimensional
 nuclear magnetic resonance spectroscopy.";
 RL Proteins 28:261-267(1997).
 -1- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
 SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS. C5-C9,
 INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
 FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYtic
 COMPLEX IS ASSEMBLED.
 -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
 C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
 POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
 MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
 -1- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC
 RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
 BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN,
 RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA
 CHAIN).
 -1- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
 -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 855
 ONWARD DUE TO THE PRESENCE OF AN ALU REPEAT.
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 DR EMBL: M57729; AAA51925.1; -;
 DR EMBL: M65134; AAA51836.1; -;
 DR PIR: A40075; CSHU.
 DR PIR: S15121; S15121.
 DR PDB: 1KJ5; 15-MAY-97.
 DR PDB: 1CFA; 17-SEP-97.
 DR Gene: HGNC:1331; C5.
 DR MIM: 120900;
 DR InterPro: IPR002890; A2M_N.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; Macroglobulin2.
 DR InterPro: IPR001134; Netrin_C.

DR Pfam: PF00207; A2M; 1.
 DR Pfam: PF01759; NTR; 1.
 DR Pfam: PF01821; ANATO; 1.
 DR Pfam: PF01835; A2M_N; 1.
 DR PRINTS: PR00004; ANAPHYLATOXN.
 DR ProDom: PD003264; Anaphylatoxin; 1.
 DR SMART: SM00104; ANATO; 1.
 DR ProDom: PD003264; Anaphylatoxin; 1.
 DR PROSITE: PS00477; ALPHA-2-MACROGLOBULIN; FALSE-NEG.
 DR PROSITE: PS01177; ANAPHYLATOXIN_2; 1.
 DR PROSITE: PS01178; ANAPHYLATOXIN_1; 1.
 KW Complement pathway; Complement alternate pathway; Glycoprotein;
 KW Plasma; Membrane attack complex; Cytolysis; Inflammatory response;
 KW Signal; Polymorphism; 3D-structure.
 FT SIGNAL 1 18
 FT CHAIN 19 673
 FT PROPEP 674 677
 FT CHAIN 678 1676
 FT PEPTIDE 678 751
 FT CHAIN 752 1676
 FT DOMAIN 698 732
 FT DISULFID 698 724
 FT DISULFID 699 731
 FT DISULFID 711 732
 FT CARBOHYD 741 741
 FT CARBOHYD 911 911
 FT CARBOHYD 1115 1115
 FT CARBOHYD 1630 1630
 FT VARIANT 518 518
 SQ SEQUENCE 1676 AA; 188331 MM; 87DCA65FF977D19 CRC64;
 Query Match 1676 AA; 95.6%; Score 109; DB 1; Length 1676;
 Best Local Similarity 95.0%; Pred. No. 3.5e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 698 CCYDGA65FF977D19
 QY 1 CCYDGA65FF977D19
 ID COSA_BOVIN STANDARD; PRT; 74 AA.
 AC P12082;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Complement C5a anaphylatoxin.
 GN C5.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-86136134; PubMed-1081348;
 RA Gennaro R., Simonic T., Negri A., Mottola C., Secchi C., Ronchi S.,
 RA Romeo D.;
 RT "C5a fragment of bovine complement. Purification, bioassays,
 RT amino-acid sequence and other structural studies.";
 RL Eur. J. Biochem. 155:77-86(1986).
 [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE-89005703; PubMed-3262536;
 RA Zarbock J., Gennaro R., Romeo D., Clore G.M., Gronenborn A.M.;
 RT "A proton nuclear magnetic resonance study of the conformation of
 RL bovine anaphylatoxin C5a in solution.";
 RL FEBS Lett. 238:289-294(1988).
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
 CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND

CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
 CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
 CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 DR PIR: A25408; A25408.
 DR HSSP: P01032; 1C5A.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; MacrogloblnA2.
 DR Pfam: PF01821; ANATO; 1.
 DR PRINTS: PR00004; ANAPHYLATOXN.
 DR ProDom: PD003264; Anaphylatoxin; 1.
 DR SMART: SM00104; ANATO; 1.
 DR PROSITE: PS00477; ALPHA_2-MACROGLOBULIN; PARTIAL.
 DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
 KW Complement pathway: Complement alternate pathway; Plasma;
 KW Inflammatory response.
 KM DOMAIN 21 55 ANAPHYLATOXIN-LIKE.
 FT DISULFID 21 47 BY SIMILARITY.
 FT DISULFID 22 54 BY SIMILARITY.
 FT DISULFID 34 55 BY SIMILARITY.
 SQ SEQUENCE 74 AA; 8517 MW; C09DF742D12D70F6 CRC64;

Query Match 82.5%; Score 94; DB 1; Length 74;
 Best Local Similarity 80.0%; Pred. No. 3.3e-08;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTCERAR 20
 DB 21 CCYDGAHRNDETCERAR 40
 ||||| |::|||::|||

RESULT 3
 COSA_PIG STANDARD; PRT; 74 AA.
 AC P01032;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Complement C5a anaphylatoxin.
 GN C5.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RP SEQUENCE.
 RX MEDLINE=80182137; PubMed=7372604;
 RA Gerard C., Hugli T.E.;
 RT "Amino acid sequence of the anaphylatoxin from the fifth component of
 RT porcine complement.";
 RL J. Biol. Chem. 255:4710-4715(1980).
 RN [2]
 RP ACTIVE REGION.
 RX MEDLINE=8119549; PubMed=6940191;
 RA Gerard C., Hugli T.E.;
 RT "Identification of classical anaphylatoxin as the des-Arg form of the
 RT C5a molecule: evidence of a modulator role for the oligosaccharide
 RT unit in human des-Arg74-C5a.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:1833-1837(1981).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=90248365; PubMed=2337573;
 RA Williamson M.P., Madison V.S.;
 RT "Three-dimensional structure of porcine C5adesArg from 1H nuclear
 RT magnetic resonance data.";
 RL Biochemistry 29:2895-2905(1990).
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
 CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF

CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
 CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 DR PIR: A01268; C5EGAT.
 DR PDB: 1C5A; 15-OCT-91.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; MacrogloblnA2.
 DR Pfam: PF01821; ANATO; 1.
 DR PRINTS: PR00004; ANAPHYLATOXN.
 DR ProDom: PD003264; Anaphylatoxin; 1.
 DR SMART: SM00104; ANATO; 1.
 DR PROSITE: PS00477; ALPHA_2-MACROGLOBULIN; PARTIAL.
 DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
 KW Complement pathway: Complement alternate pathway; Plasma;
 KW Inflammatory response; 3D-structure.
 KM DOMAIN 21 55 ANAPHYLATOXIN-LIKE.
 FT DISULFID 21 47
 FT DISULFID 22 54
 FT DISULFID 34 55
 FT SITE 72 74
 FT HELIX 2 11
 FT TURN 13 14
 FT HELIX 16 26
 FT HELIX 34 40
 FT HELIX 45 62
 FT TURN 63 64
 SQ SEQUENCE 74 AA; 8609 MW; 11AAFE294A026EB3 CRC64;

Query Match 81.6%; Score 93; DB 1; Length 74;
 Best Local Similarity 80.0%; Pred. No. 4.8e-08;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTCERAR 20
 DB 21 CCYDGAHRNDETCERAR 40
 ||||| |::|||::|||

RESULT 4
 COSA_RAT STANDARD; PRT; 76 AA.
 AC P08650;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Complement C5a anaphylatoxin.
 GN C5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RA Cui L.-X., Ferreri K., Hugli T.E.;
 RT "Characterization of rat C5a, a uniquely active spasmogen.";
 RL Complement 2:18-19(1985).
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
 CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
 CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
 CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 DR HSSP: P01031; 1KJS.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; MacrogloblnA2.
 DR Pfam: PF01821; ANATO; 1.
 DR PRINTS: PR00004; ANAPHYLATOXN.
 DR ProDom: PD003264; Anaphylatoxin; 1.

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DR SMART: SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA-2-MACROGLOBULIN; PARTIAL.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway; Complement alternate pathway; Glycoprotein;
KW Plasma; Inflammatory response.
FT DOMAIN 24 58
FT DISULFID 24 50 ANAPHYLATOXIN-LIKE.
FT DISULFID 25 57 BY SIMILARITY.
FT DISULFID 37 58 BY SIMILARITY.
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .);
SQ SEQUENCE 76 AA; 8869 MW; 2EC15183A6B54769 CRC64;

Query Match 73.7%; Score 84; DB 1; Length 76;
Best Local Similarity 75.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CCYDGSVNNDECEQRAAR 20
DB 24 CCYDGAENRYETCEQRYAR 43

RESULT 5
COS_MOUSE STANDARD; PRT; 1680 AA.
AC P0684;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Complement C5 precursor (Hemolytic complement) [Contains: C5A
DE anaphylatoxin].
GN C5 OR HC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90153853; PubMed=2303408;
RA Wetsel R.A., Fleischer D.T., Haviland D.L.;
RT "Deficiency of the murine fifth complement component (C5). A 2-base
RT pair gene deletion in a 5'-exon.";
RN J. Biol. Chem. 265:2435-2440(1990).
RP
RX SEQUENCE OF 41-1680 FROM N.A.
RX MEDLINE=87185363; PubMed=2436653;
RA Wetsel R.A., Ogata R.T., Tack B.F.;
RT "Primary structure of the fifth component of murine complement.";
RN Biochemistry 26:737-743(1987).
CC -1- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
CC SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,
CC INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
CC FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYtic
CC COMPLEX IS ASSEMBLED.
CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
CC -1- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC
CC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA. LINKED BY A DISULFIDE
CC BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN,
CC RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA
CC CHAIN).
CC -1- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
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CC -----
DR EMBL; M35525; AAA37349.1; -.
DR EMBL; M35526; AAA37348.1; -.
DR PIR; A27538; A27538.
DR PIR; A35530; A35530.
DR HSSP; P01031; 1KJS.
DR MGD; MGI:96031; HC.
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001840; Anaphylatoxin.
DR InterPro; IPR001599; MacrogloblnA2.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01759; NTR; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01835; A2M_N; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR PRODOM; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA-2-MACROGLOBULIN; FALSE_NEG.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway; Complement alternate pathway; Glycoprotein;
KW Plasma; Membrane attack complex; Cytolysis; Inflammatory response;
KW Signal.
FT SIGNAL 1 18
FT CHAIN 19 1680 COMPLEMENT C5.
FT CHAIN 19 674 COMPLEMENT C5 BETA CHAIN.
FT PROPEP 675 678 COMPLEMENT C5 ALPHA CHAIN.
FT CHAIN 679 1680 C5A ANAPHYLATOXIN.
FT PEPTIDE 679 755 C5B (ALPHA).
FT CHAIN 756 1680 ANAPHYLATOXIN-LIKE.
FT DOMAIN 702 736 BY SIMILARITY.
FT DISULFID 702 728 BY SIMILARITY.
FT DISULFID 715 736 BY SIMILARITY.
FT CARBOHYD 427 427 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 915 915 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1119 1119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1633 1633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 216 216 Y -> L (IN DEFECTIVE VARIANT C5D).
FT VARIANT 217 1680 MISSING (IN DEFECTIVE VARIANT C5D).
SQ SEQUENCE 1680 AA; 188877 MW; 81B55A16FAC7D95C CRC64;

Query Match 73.7%; Score 84; DB 1; Length 1680;
Best Local Similarity 75.0%; Pred. No. 3e-05;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCYDGSVNNDECEQRAAR 20
DB 702 CCYDGAENRYETCEQRYAR 721

RESULT 6
COS_MOUSE STANDARD; PRT; 1738 AA.
AC P01029; Q61859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Complement C4 precursor [Contains: C4a anaphylatoxin].
GN C4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85298264; PubMed=3862104;
RA Sepich D.S., Noonan D.J., Ogata R.T.;

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RT "Complete cDNA sequence of the fourth component of murine
 RT complement.",
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5895-5899(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B12.WR;
 RX MEDLINE=87309760; PubMed=3624865;
 RA Rosa P.A., Sepich D.S., Robins D.M., Ogata R.T.;
 RT "Constitutive expression of SLP genes in mouse strain B10.WR directed
 RT by C4 regulatory sequences.";
 RL J. Immunol. 139:1568-1577(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B12.WR; TISSUE=Liver;
 RX MEDLINE=89380278; PubMed=2777798;
 RA Ogata R.T., Rosa P.A., Zepf N.E.;
 RT "Sequence of the gene for murine complement component C4.";
 RL J. Biol. Chem. 264:16565-16572(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FW; TISSUE=Liver;
 RX MEDLINE=85289294; PubMed=2993295;
 RA Nonaka M., Nakayama K., Yeul Y.D., Takahashi M.;
 RT "Complete nucleotide and derived amino acid sequences of the fourth
 RT component of mouse complement (C4). Evolutionary aspects.";
 RL J. Biol. Chem. 260:10936-10943(1985).
 RN [5]
 RP SEQUENCE OF 651-810 AND 924-1083 FROM N.A.
 RX MEDLINE=85038607; PubMed=6208559;
 RA Nonaka M., Takahashi M., Natsunume-Sakai S., Nonaka M., Tanaka S.,
 RA Shimizu A., Hoojo T.;
 RT "Isolation of cDNA clones specifying the fourth component of mouse
 RT complement and its isotype, sex-limited protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6822-6826(1984).
 RN [6]
 RP SEQUENCE OF 1099-1142 FROM N.A.
 RC STRAIN-B10.WR, C57BL/6, C3H/He, CBA/J, B10.BR, and DBA2;
 RX MEDLINE=90353398; PubMed=2387317;
 RA Ogata R.T., Zepf N.E.;
 RT "C4 from C4-high and C4-low mouse strains have identical sequences in
 RT the region corresponding to the isotype-specific segment of human
 RT C4.";
 RL Eur. J. Immunol. 20:1607-1610(1990).
 RN [7]
 RP SEQUENCE OF 1105-1449 FROM N.A.
 RX MEDLINE=95166208; PubMed=3856857;
 RA Levi-Strauss M., Tosi M., Steinmetz M., Klein J., Meo T.;
 RT "Multiple duplications of complement C4 gene correlate with H-2-
 RT controlled testosterone-independent expression of its sex-limited
 RT isoform, C4-SLP.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:1746-1750(1985).
 RN [8]
 RP SEQUENCE OF 1257-1376 FROM N.A.
 RX MEDLINE=95038859; PubMed=6149581;
 RA Tosi M., Levi-Strauss M., Duponchel C., Meo T.;
 RT "Sequence heterogeneity of murine complementary DNA clones related to
 RT the C4 and C4-SLP isoforms of the fourth complement component.";
 RL Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:389-394(1984).
 RN [9]
 RP SEQUENCE OF 1360-1511 FROM N.A.
 RX MEDLINE=83273751; PubMed=6192448;
 RA Ogata R.T., Shreffler D.C., Sepich D.S., Lilly S.P.;
 RT "cDNA clone spanning the alpha-gamma subunit junction in the
 RT precursor of the murine fourth complement component (C4)."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:5061-5065(1983).
 RN [10]
 RP SEQUENCE OF 1-128 FROM N.A.
 RC STRAIN-FW; TISSUE=Liver;
 RX MEDLINE=86031969; PubMed=2997024;
 RA Nonaka M., Nakayama K., Yeul Y.D., Shimizu A., Takahashi M.;
 RT "Molecular cloning and characterization of complementary and genomic
 RT DNA clones for mouse C4 and SLP.";
 RL Immunol. Rev. 87:81-99(1985).

RN [11]
 RP SEQUENCE OF 1-21 FROM N.A.
 RX MEDLINE=87017050; PubMed=3464002;
 RA Nonaka M., Kimura H., Yeul Y.D., Yokoyama S., Nakayama K.,
 RA Takahashi M.;
 RT "Identification of the 5'-flanking regulatory region responsible for
 RT the difference in transcriptional control between mouse complement C4
 RT and SLP genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:7883-7887(1986).
 RN [12]
 RP FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
 CC CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY
 CC ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A
 CC ANAPHYLATOXIN.
 CC -1- SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR
 CC AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER
 CC OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).
 CC -1- MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
 CC PROTEIN.
 CC -1- SIMILARITY: TO C3, C5 AND ALPHA-2-MACROGLOBULIN.
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: K00019; AAA39554.1; -
 DR EMBL: M11729; AAA39506.1; -
 DR EMBL: M12968; AAA39558.1; -
 DR EMBL: M12970; AAA39555.1; -
 DR EMBL: M12972; AAA39556.1; -
 DR EMBL: M12969; AAA39557.1; -
 DR EMBL: M11789; AAA39557.1; -
 DR EMBL: K02798; AAC42021.1; -
 DR EMBL: M17440; AAA39561.1; -
 DR EMBL: M14225; AAA39563.1; -
 DR EMBL: M14226; AAA39684.1; -
 DR EMBL: X55493; CAA39112.1; -
 DR EMBL: X55495; CAA39114.1; -
 DR PIR: A01264; A01264.
 DR PIR: A21692; A21692.
 DR PIR: A22039; A22039.
 DR PIR: A24558; A24558.
 DR PIR: A29059; A29059.
 DR HSP: P01031; 1KJ5.
 DR MGD: MGI:88228; C4.
 DR InterPro: IPR002890; A2M_N.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; Macroglobulin2.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF00207; A2M; 1.
 DR Pfam: PF01759; NTR; 1.
 DR Pfam: PF01821; ANATO; 1.
 DR Pfam: PF01835; A2M_N; 1.
 DR PRINTS: PR00004; ANAPHYLATOXN.
 DR PRODOM: PD003264; Anaphylatoxin; 1.
 DR SMART: SM00104; ANATO; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
 KW Complement pathway; Plasma; Glycoprotein; Sulfation; Signal;
 KW Inflammatory response.
 FT SIGNAL 1 19
 FT CHAIN 20 673
 FT PROPEP 674 677
 FT CHAIN 678 1443
 FT PROPEP 1444 1447
 FT CHAIN 1448 1738
 FT PEPTIDE 678 753
 FT
 CC COMPLEMENT C4, BETA CHAIN.
 CC COMPLEMENT C4, ALPHA CHAIN.
 CC COMPLEMENT C4, GAMMA CHAIN.
 CC C4A ANAPHYLATOXIN.

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FT DOMAIN 700 734 ANAPHYLATOXIN-LIKE.
FT DISULFID 700 726 BY SIMILARITY.
FT DISULFID 701 733 BY SIMILARITY.
FT DISULFID 714 734 BY SIMILARITY.
FT THIOLEST 1006 1009 BY SIMILARITY.
FT MOD_RES 1413 1413 SULFATION.
FT MOD_RES 1416 1416 SULFATION.
FT MOD_RES 1417 1417 SULFATION.
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 743 743 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1387 1387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 132 132 F -> Y (IN REF. 4).
FT CONFLICT 327 327 G -> E (IN REF. 4).
FT CONFLICT 570 570 G -> E (IN REF. 4).
FT CONFLICT 720 720 R -> G (IN REF. 5).
FT CONFLICT 739 740 DL -> AI (IN REF. 5).
FT CONFLICT 838 838 P -> R (IN REF. 4).
FT CONFLICT 993 993 P -> L (IN REF. 5).
FT CONFLICT 1043 1043 D -> E (IN REF. 5).
FT CONFLICT 1119 1119 V -> A (IN REF. 7).
FT CONFLICT 1190 1190 A -> T (IN REF. 7).
FT CONFLICT 1324 1324 K -> S (IN REF. 4).
FT CONFLICT 1401 1401 G -> N (IN REF. 9).
FT CONFLICT 1442 1442 R -> K (IN REF. 4).
FT CONFLICT 1453 1453 A -> V (IN REF. 4).
SQ SEQUENCE 1738 AA; 192870 MW; D1EE02AETAB42BFF CRC64;

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Query Match 49.68; Score 56.5; DB 1; Length 1738;
Best Local Similarity 57.18; Pred. No. 0.67;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

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OY 1 CCYDG-ASVNNDETCERAR 20
DB 700 CCODGWTXLPKMRTECERAR 720

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RESULT 7
CO4_RAT STANDARD; PRT; 76 AA.
AC P08649;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Complement C4a anaphylatoxin.
GN C4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=8834568; PubMed=3262196;
RA Cui L.-X., Ferreri K., Hugli T.E.;
RT "Structural characterization of the C4a anaphylatoxin from rat.";
RL Mol. Immunol. 25:663-671(1988).
RN [2]
RP SEQUENCE.
RA Cui L.-X., Ferreri K., Hugli T.E.;
RT "Characterization of rat anaphylatoxins C4a and C5a.";
RL Fed. Proc. 44:991-991(1985).
CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C4,
CC C4A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC BASOPHILIC LEUKOCYTES.
CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
DR HSP; P01036; J00036.
DR HSP; P01031; IJ03.
DR InterPro: IPR000020; Anaphylatoxin.
DR InterPro: IPR001840; Anaphylatoxin.
DR InterPro: IPR001599; MacroglobulinA2.
DR Pfam: PF01821; ANATO; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.

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DR ProDom: PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; PARTIAL.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway; Plasma; Inflammatory response; Glycoprotein.
FT DOMAIN 23 57 ANAPHYLATOXIN-LIKE.
FT DISULFID 23 49 BY SIMILARITY.
FT DISULFID 24 56 BY SIMILARITY.
FT DISULFID 37 57 BY SIMILARITY.
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .).
FT CONFLICT 29 29 T -> A (IN REF. 2).
SQ SEQUENCE 76 AA; 8594 MW; 96700DB7AFB7C6DB CRC64;

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OY 1 CCYDG-ASVNNDETCERAR 20
DB 23 CCODGWTXLPKMRTECERAR 43

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Query Match 48.78; Score 55.5; DB 1; Length 76;
Best Local Similarity 57.18; Pred. No. 0.039;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

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RESULT 8
CO4_BOVIN STANDARD; PRT; 920 AA.
AC P01030; Q27993; Q27992;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Complement C4 precursor [Contains: C4a anaphylatoxin] (Fragments).
GN C4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP MEDLINE=83126436; PubMed=6760852;
RA Smith M.A., Gerlie L.M., Dunbar B., Fothergill J.E.;
RT "Primary structure of bovine complement activation fragment C4a, the
RT third anaphylatoxin. Purification and complete amino acid sequence.";
RL Biochem. J. 207:253-260(1982).
RN [2]
RP SEQUENCE OF 78-920 FROM N.A.
RC TISSUE=Liver;
RA Groth D.M.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
CC CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY
CC ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A
CC ANAPHYLATOXIN.
CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C4,
CC C4A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC BASOPHILIC LEUKOCYTES.
CC -1- SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR
CC AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER
CC OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).
CC -1- MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
CC PROTEIN.
CC -1- SIMILARITY: TO C3, C5 AND ALPHA-2-MACROGLOBULIN.
CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
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DR	PROSITE: PS01178; ANAPHYLATOXIN 2; 1.
KW	Complement pathway; Plasma; Glycoprotein; Sulfation; Signal;
KW	Inflammatory response; Polymorphism; Disease mutation;
KW	Blood group antigen.
FT	SIGNAL 1 19
FT	CHAIN 20 675
FT	PROPEP 676 679
FT	CHAIN 680 1446
FT	PROPEP 1447 1453
FT	CHAIN 1454 1744
FT	PEPTIDE 680 756
FT	DOMAIN 702 736
FT	DISULFID 702 728
FT	DISULFID 703 735
FT	DISULFID 716 736
FT	THIOLEST 1010 1013
FT	MOD_RES 1417 1417
FT	MOD_RES 1420 1420
FT	MOD_RES 1422 1422
FT	CARBOHYD 226 226
FT	CARBOHYD 862 862
FT	CARBOHYD 1328 1328
FT	CARBOHYD 1391 1391
FT	VARIANT 477 477
FT	VARIANT 726 726
FT	VARIANT 1073 1073
FT	VARIANT 1073 1073

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QY      1 CCYGAS-VNNDTCBORAR 20          45.2%   Score 51.5; DB 1; Length 1744;
        ||| : : :|||
Db       702 CCGDGTRLPMRSCQRRA 722         Pred. No. 4.1;
Matches  11; Conservative     3; Mismatches    6; Indels    1; Gaps    1

RESULT 10
V32K_BNYG
ID      V32K_BNYVG           STANDARD:      PRT;      282 AA.
AC      P19231;
DT      01-NOV-1990 (Rel. 16, Created)
DI      01-NOV-1990 (Rel. 16, Last sequence update)
DR      01-NOV-1990 (Rel. 16, Last annotation update)
DE      RNA-4 hypothetical 31.9 kDa protein.
OS      Beet necrotic yellow vein mosaic virus (isolate GI).
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX      NCBI_TaxID=12257;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Bouzouba S., Guillely H., Jonard G., Richards K., Putz C.;
RT      "Nucleotide sequence analysis of RNA-3 and RNA-4 of beet necrotic
RL      yellow vein virus, isolates F2 and GI."
RJ      J. Gen. Virol. 66:1553-1564(1985).
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@ebi.ac.uk).
CC      -----
DR      EMBL: M36897; AAAA2800.1; .
KW      Hypothetical protein.
SQ      SEQUENCE 282 AA; 31869 MW; AA7C0351CA54FE0CC CRC64;

Query Match          42.1%; Score 48; DB 1; Length 282;
Best Local Similarity 57.1%; Pred. No. 2.3;
Matches      8; Conservative     1; Mismatches    5; Indels    0; Gaps    0;
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OY 2 CYDASVNDDETC 15
 DB 115 CYSQVYSLDELCE 128

RESULT 11

OVOS_CHICK STANDARD: PRT: 1473 AA.
 ID OVOS_CHICK
 AC P20740;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Ovocystin precursor (Ovocystoglobulin).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oviduct;
 RX MEDLINE=95218210; PubMed=7535598;
 RA Nielsen K.L., Soltrop-Jensen L., Nagase H., Thøgersen H.C.,
 RT Etxerodt M.;
 RT "Amino acid sequence of hen ovomacroglobulin (ovocystin) deduced from
 RT cloned cDNA.";
 RL DNA Seq. 5:111-119(1994).
 RN [2]
 RP SEQUENCE OF 37-49.
 RC TISSUE=Egg white;
 RX MEDLINE=83238315; PubMed=6408074;
 RA Nagase H., Harris E.D. Jr., Woessner J.F., Brew K.;
 RT "Ovocystin: a novel proteinase inhibitor from chicken egg white. I.
 RT Purification, physicochemical properties, and tissue distribution of
 RT ovomacroglobulin.";
 RL J. Biol. Chem. 258:7481-7489(1983).
 RN [3]
 RP SEQUENCE OF 976-1028.
 RC TISSUE=Egg white;
 RX MEDLINE=93192299; PubMed=7680577;
 RA Nielsen K.L., Soltrop-Jensen L.;
 RT "Evidence from sequence analysis that hen egg-white ovomacroglobulin
 RT (ovocystin) is devoid of an internal beta-Cys-gamma-Glu thiol
 RT ester.";
 RL Biochim. Biophys. Acta 1162:230-232(1993).
 CC -1- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A
 CC UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH
 CC CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES
 CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT
 CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH
 CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST
 CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR
 CC WEIGHT SUBSTRATES IS GREATLY REDUCED).
 CC -1- SUBUNIT: HOMOTETRAMER, WHICH CONSISTS OF TWO PAIRS OF DISULFIDE-
 CC LINKED CHAINS.
 CC -1- PTM: THIS PROTEIN LACKS THE THIOESTER BOND FOUND IN OTHER MEMBERS
 CC OF THIS FAMILY.
 CC -1- PTM: CONTAINS 56 MOL. GLUCOSAMINE PER MOL. SUBUNIT.
 CC -1- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
 CC -----
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 CC -----
 CC EMBL: X78801; CAA55384.1; -
 CC EMBL: X78801; CAA55385.1; ALT_INIT.
 CC PIR: A20872; A20872.
 CC HSP: P01023; IBAV.

DR InterPro: IPR002890; A2M_N.
 DR InterPro: IPR001599; MacroglublnA2.
 DR Pfam: PF00207; A2M; 1.
 DR Pfam: PF01835; A2M_N; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; FALSE_NEG.
 KW Serine protease inhibitor; Glycoprotein; Bait region; Signal.
 FT SIGNAL 1 36
 FT CHAIN 37 1473
 FT CARBOHYD 67 67 OVOSTATIN.
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 588 588 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 757 757 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1141 1141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1221 1221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1315 1315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1347 1347 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 46 46 M -> V (IN REF. 2).
 SO SEQUENCE 1473 AA; 166354 MW; A33C6847A14179BF CRC64;

Query Match 40.4%; Score 46; DB 1; Length 1473;
 Best local similarity 53.3%; Pred. No. 25;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 6 ASVNDDETCQRRAR 20
 DB 883 AETNDDEACEEALR 897

RESULT 12

ID Y125_MYCPN STANDARD: PRT: 281 AA.
 AC P75511;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MG125 homolog (A65_01281).
 GN MPN264 OR MPN569.
 OS Mycoplasma pneumoniae.
 CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelfreisch R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- SIMILARITY: BELONGS TO THE COF/YBHA/YIDA/YIGL (E.COLI) / YCSE/YXEH
 CC (B.SUBTILIS) FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE000056; AAB96217.1; -
 CC InterPro: IPR001454; Hlygase/hygrase.
 CC InterPro: IPR001510; Hypothet_cof.
 CC Pfam: PF00702; Hydrolase; 1.
 CC PROSITE: PS01228; COF-1; 1.
 CC PROSITE: PS01229; COF-2; 1.
 CC Hypothetical protein; Complete proteome.
 SO SEQUENCE 281 AA; 32614 MW; BF44564E7C7FBF11 CRC64;

Query Match 39.0%; Score 44.5; DB 1; Length 281;
 Best Local Similarity 47.4%; Pred. No. 8.1;
 Matches 9; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 1 CCYGA---SVNDETCBO 16
 ||| | :||: ||
 Db 71 CCYGAALYQLNNNPQEQ 89

RESULT 13
 ID CFAH_BOVIN STANDARD; PRT; 685 AA.
 AC Q28085;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Complement factor H (H factor 1) (Fragments).
 GN HPI.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 17-685 FROM N.A., AND SEQUENCE OF 1-16.
 RC TISSUE=Liver;
 RA MEDLINE=96202005; PubMed=6615824;
 RX Soames C.J., Day A.J., Sim R.B.;
 RT "Prediction from sequence comparisons of residues of factor H involved in the interaction with complement component C3b.";
 RL Biochem. J. 315:523-531(1996).
 CC -I- FUNCTION: Factor H functions as a cofactor in the inactivation of C3b by factor I and also increases the rate of dissociation of the C3bB complex (C3 convertase) and the (C3b)NBB complex (C5 convertase) in the alternative complement pathway (By similarity).
 CC -I- SIMILARITY: CONTAINS AT LEAST 13 SUSHI (SCR) DOMAINS.
 CC -----
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 CC -----
 CC EMBL: X98697; CAA67257.1; -
 DR HSSP: P10998; IYVD.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00084; sushi_11.
 DR SMART: SM00032; CCP; 11.
 DR Complement alternate pathway; Plasma; Repeat; Sushi.
 KW NON_TER
 FT NON_TER 1 1
 FT DOMAIN 16 17
 FT DOMAIN <17 67 SUSHI 2.
 FT DOMAIN 70 131 SUSHI 3.
 FT DOMAIN 134 188 SUSHI 4.
 FT DOMAIN 191 246 SUSHI 5.
 FT DOMAIN 249 309 SUSHI 6.
 FT DOMAIN 311 366 SUSHI 7.
 FT DOMAIN 370 429 SUSHI 8.
 FT DOMAIN 431 488 SUSHI 9.
 FT DOMAIN 491 547 SUSHI 10.
 FT DOMAIN 553 609 SUSHI 11.
 FT DOMAIN 614 668 SUSHI 12.
 FT DOMAIN 675 >685 SUSHI 13.
 FT DISULFID 39 66 BY SIMILARITY.
 FT DISULFID 71 117 BY SIMILARITY.
 FT DISULFID 103 130 BY SIMILARITY.
 FT DISULFID 135 176 BY SIMILARITY.
 FT DISULFID 162 187 BY SIMILARITY.
 FT DISULFID 192 234 BY SIMILARITY.
 FT DISULFID 219 245 BY SIMILARITY.
 DR

FT DISULFID 250 297 BY SIMILARITY.
 FT DISULFID 280 308 BY SIMILARITY.
 FT DISULFID 312 354 BY SIMILARITY.
 FT DISULFID 339 365 BY SIMILARITY.
 FT DISULFID 371 417 BY SIMILARITY.
 FT DISULFID 400 428 BY SIMILARITY.
 FT DISULFID 432 476 BY SIMILARITY.
 FT DISULFID 459 487 BY SIMILARITY.
 FT DISULFID 492 534 BY SIMILARITY.
 FT DISULFID 520 546 BY SIMILARITY.
 FT DISULFID 554 597 BY SIMILARITY.
 FT DISULFID 583 608 BY SIMILARITY.
 FT DISULFID 615 656 BY SIMILARITY.
 FT DISULFID 642 667 BY SIMILARITY.
 FT NON_TER 685 685 BY SIMILARITY.
 SO SEQUENCE 685 AA; 77536 MW; 69FC9DC8D530E872 CRC64;

Query Match 39.0%; Score 44.5; DB 1; Length 685;
 Best Local Similarity 44.4%; Pred. No. 20;
 Matches 8; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 2 CYDGA---SVNDETCBO 16
 ||| | :||: ||
 Db 339 CYDGAALYQLNNNPQEQ 356

RESULT 14
 ID YLJ9_CABEL STANDARD; PRT; 1205 AA.
 AC P34372;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C50C3.9 in chromosome III precursor.
 GN C50C3.9.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol NZ;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Kershaw J., Kilsten J., Laisler N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhan R., Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Welstock L., Wilkinson-Sproat J., Wohldman P.;
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
 RT Nature 368:32-38(1994).
 RN [2]
 RP REVISIONS.
 RA Waterston R.;
 CC Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: CONTAINS 1 WFPA DOMAIN.
 CC -----
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 CC -----
 CC EMBL: L14433; AAA27971.2; -
 DR PIR: S44619; S44619.

DR WormRep: C50C3.9; CE24860.
 DR InterPro: IPR002035; VFMA.
 DR Pfam: PF00092; VMA; 1.
 DR Pfam: PF02743; Cache; 1.
 DR SMART: SM00327; VMA; 1.
 KM Hypothetical protein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 1205
 FT DOMAIN 250 435
 FT SEQUENCE 1205 AA; 139339 MW; 79A2F96C052BF91C CRC64;
 VFMA.
 CHROMOSOME III.
 Query Match 39.0%; Score 44.5; DB 1; Length 1205;
 Best Local Similarity 29.4%; Pred. No. 36;
 Matches 10; Conservative 3; Mismatches 6; Indels 15; Gaps 1;
 QY 2 CYDGA-----SYNDETCEORAR 20
 DB 1126 CYDESECSMELSNVPRGFEEVKNETCEENK 1159

RESULT 15
 S141_HUMAN STANDARD; PRT; 715 AA.
 ID S141_HUMAN STANDARD; PRT; 715 AA.
 AC 092503; 099780;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE SEC14-like protein 1.
 GN SEC14L1 OR SEC14L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=96302338; PubMed=8697811;
 RA Chinen K., Takahashi E., Nakamura Y.;
 RT Isolation and mapping of a human gene (SEC14L), partially homologous
 RT to yeast SEC14, that contains a variable number of tandem repeats
 RT (VNR) site in its 3' untranslated region.";
 RL Cytogenet. Cell Genet. 73:218-223(1996).
 RN [2]
 RP SEQUENCE OF 423-715 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97264341; PubMed=9110174;
 RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
 RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
 RT Large-scale concatenation cDNA sequencing.";
 RL Genome Res. 7:353-358(1997).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -1- SIMILARITY: CONTAINS 1 CRAL-TRIO DOMAIN.
 CC
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 CC
 CC EMBL: D67029; BAAL1048.1; -;
 DR EMBL: D67029; BAAL1048.1; -;
 DR EMBL: 079284; AAB50220.1; -;
 DR Genew: HGNC:10698; SEC14L1.
 DR MIM: 601504; -;
 DR InterPro: IPR001251; CRAL-TRIO.
 DR Pfam: PF00650; CRAL-TRIO; 1.
 DR SMART: SM00516; SEC14; 1.
 DR PROSITE: PSS0191; CRAL-TRIO; 1.
 DR DOMAIN 319 495
 FT DOMAIN 319 495
 FT CONFLICT 715 715 R -> RWRC (IN REF. 2).

SO SEQUENCE 715 AA; 81277 MW; F35B08C8ADE79A CRC64;
 Query Match 38.6%; Score 44; DB 1; Length 715;
 Best Local Similarity 42.1%; Pred. No. 25;
 Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 1 CCYDGA SYNDETCEORAA 19
 DB 112 CCYTVHPENEDWTCFEQSA 130
 Search completed: May 1, 2003, 22:17:44
 Job time : 13 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:15:16 ; Search time 84 Seconds

(without alignments)
49.059 Million cell updates/sec

Title: US-09-651-685a-5

Sequence: 1 CCYDGASVNNDETCEQRAAR 20

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-rvivirus:*
16: SP-bacteriap:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	73.7	77	11	063078
2	56.5	49.6	1148	11	061372
3	56.5	49.6	1738	11	070346
4	51	44.7	608	5	09V174
5	50.5	44.3	1614	13	098977
6	49.5	43.4	548	5	09M497
7	48	42.1	135	12	085686
8	48	42.1	282	12	09DGS5
9	48	42.1	282	12	09DGS4
10	48	42.1	282	12	09DGS5
11	48	42.1	282	12	09DGS5
12	48	42.1	282	12	09DGS5
13	48	42.1	282	12	09DGS5
14	47.5	41.7	282	12	065670
15	47	41.2	1684	13	09DVS9
16	47	41.2	227	5	09GT77
			834	12	085429

17	47	41.2	834	12	085430	085430 rice stripe
18	47	41.2	1625	12	055597	055597 garlic viru
19	46	40.4	265	16	08X554	08X554 clostridium
20	45.5	39.9	1159	13	09Y1A6	09Y1A6 cyprinus ca
21	45.5	39.9	1640	13	09Y1A8	09Y1A8 cyprinus ca
22	45.5	39.9	1642	13	09Y1B0	09Y1B0 cyprinus ca
23	45.5	39.9	1642	13	09Y1B0	09Y1B0 cyprinus ca
24	45	39.5	159	16	09CG11	09CG11 lactococcus
25	45	39.5	163	12	09J813	09J813 spodoptera
26	45	39.5	221	5	09NL25	09NL25 plasmodium
27	45	39.5	226	5	09N6J1	09N6J1 plasmodium
28	45	39.5	226	5	09N6G5	09N6G5 plasmodium
29	45	39.5	226	5	09NL21	09NL21 plasmodium
30	45	39.5	226	5	09G556	09G556 plasmodium
31	45	39.5	231	5	09N681	09N681 plasmodium
32	45	39.5	231	5	09N673	09N673 plasmodium
33	45	39.5	231	5	09NL24	09NL24 plasmodium
34	45	39.5	231	5	09NL23	09NL23 plasmodium
35	45	39.5	231	5	09NL22	09NL22 plasmodium
36	45	39.5	231	5	09NL20	09NL20 plasmodium
37	45	39.5	231	5	09NL19	09NL19 plasmodium
38	45	39.5	236	5	09NL18	09NL18 plasmodium
39	45	39.5	282	12	09DS77	09DS77 beet necrot
40	45	39.5	394	5	093521	093521 caenorhabdi
41	45	39.5	739	2	087381	087381 haemophilus
42	44.5	39.0	1589	13	091588	091588 xenopus lae
43	44.5	39.0	1700	13	091933	091933 cyprinus ca
44	44	38.6	68	16	08YTK5	08YTK5 bruceella me
45	44	38.6	285	12	09Z015	09Z015 garlic viru

ALIGNMENTS

RESULT 1	ID	063078	PREDIMINARY:	PRT:	77 AA.
AC	063078;	063078;			
DT	01-NOV-1996 (TREMblrel. 01, Created)				
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)				
DT	01-OCT-2001 (TREMblrel. 18, Last annotation update)				
DE	Cca complement component protein (Fragment).				
GN	Csa.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_TaxID=10116;				
RP	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-LEWIS; TISSUE=LIVER;				
RX	MEDLINE-97236424; PubMed-9116048;				
RA	Rothermel E., Rolf O., Goetze O., Zwirner J.;				
RT	"Nucleotide and corrected amino acid sequence of the functional				
RT	recombinant rat anaphylatoxin Csa."				
RL	Biochim. Biophys. Acta 1351:9-12(1997).				
DR	EMBL; X91892; CAA62994.1; -				
DR	HSSP; P01031; 1KJ5.				
DR	InterPro: IPR000020; Anaphylatoxin.				
DR	InterPro: IPR001840; Anaphylatoxin.				
DR	Pfam; PF01821; ANATO.1.				
DR	PRINTS; PR00004; ANAPHYLATOXN.				
DR	ProDom; PD003264; Anaphylatoxin; 1.				
DR	SMART; SM00104; ANATO.1.				
DR	PROSITE; PS01177; ANAPHYLATOXIN_1; 1.				
DR	PROSITE; PS01178; ANAPHYLATOXIN_2; 1.				
FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE	77 AA; 8981 MW; 14141F41C38BD28 CRC64;			
Query Match		73.7%; Score 84; DB 11; Length 77;			
Best Local Similarity		75.0%; Pred. No. 1.2e-06;			
Matches	15; Conservative	0; Mismatches 5; Indels 0; Gaps 0;			

OY 1 CCYDGSVNNDETCEQRRAR 20
 ||||| 1 ||||| 1
 Db 24 CCYDGSVNNDETCEQRRAR 43

RESULT 2

061372 PRELIMINARY; PRT: 1148 AA.

AC 061372;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE C4 complement protein (Fragment).

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]

SEQUENCE FROM N.A.

RC STRAIN-B10.D2(C4(H)SLP(A));
 RX MEDLINE=86176748; PubMed=3008092;
 RA Hemenway C., Kalif M., Stavenhagen J., Walthall D., Robins D.;
 RT "Sequence comparison of alleles of the fourth component of complement
 (C4) and sex-limited protein (SLP).";
 RL Nucleic Acids Res. 14:2539-2554(1986).
 DR EMU: X05314; CAA28936.1; -.
 DR HSSP: P01031; 1KJS.

DR MGD: MGI:88228; C4.
 DR InterPro: IPR002890; A2M_N.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; MacroglobinA2.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF00207; A2M; 1.
 DR Pfam: PF01835; A2M_N; 1.
 DR Pfam: PF01821; ANATO; 1.
 DR Pfam: PF01759; NTR; 1.
 DR PRINTS: PR00004; ANAPHYLATOXN.
 DR ProDom: PD003264; Anaphylatoxin; 1.
 DR SMART: SM00104; ANATO; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 1148 AA; 127361 MW; 2710ECF832B6FC9 CRC64;

Query Match 49.6%; Score 56.5; DB 11; Length 1148;
 Best Local Similarity 57.1%; Pred. No. 0.99;
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

OY 1 CCYDGSVNNDETCEQRRAR 20
 ||||| 1 ||||| 1
 Db 110 CCYDGSVNNDETCEQRRAR 130

RESULT 3

070346 PRELIMINARY; PRT: 1738 AA.

AC 070346;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Complement C4.
 GN STR19 OR C4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]

RP SEQUENCE FROM N.A.
 RA Krown L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas G.,
 RA Hood L.; 3

RT "Sequence of the mouse major histocompatibility locus class III
 region.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF049850; AAC05279.1; -.
 DR HSSP: P01031; 1KJS.

DR MGD: MGI:1860085; SK19.
 DR MGD: MGI:88228; C4.
 DR InterPro: IPR002890; A2M_N.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; MacroglobinA2.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF00207; A2M; 1.
 DR Pfam: PF01835; A2M_N; 1.
 DR Pfam: PF01821; ANATO; 1.
 DR Pfam: PF01759; NTR; 1.
 DR PRINTS: PR00004; ANAPHYLATOXN.
 DR ProDom: PD003264; Anaphylatoxin; 1.
 DR SMART: SM00104; ANATO; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
 SQ SEQUENCE 1738 AA; 192944 MW; BDD82802091EE81 CRC64;

Query Match 49.6%; Score 56.5; DB 11; Length 1738;
 Best Local Similarity 57.1%; Pred. No. 1.6;
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

OY 1 CCYDGSVNNDETCEQRRAR 20
 ||||| 1 ||||| 1
 Db 700 CCYDGSVNNDETCEQRRAR 720

RESULT 4

09V174 PRELIMINARY; PRT: 608 AA.

AC 09V174;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE CG10055 protein.

GN CG10055.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chape M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaslev E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fodor C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostali D., Houston K.A., Howland T.J., Wei M.-H., Ibegyan C.,
 RA Jaisl M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merklov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacile J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tecor C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weisslock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003672; AAF54051.1; -;
 DR FLYBASE: FBgn0037482; CC10055.
 SQ SEQUENCE 608 AA; 69145 MW; 0357365F2567014 CRC64;

Query Match 44.7%; Score 51; DB 5; Length 608;
 Best Local Similarity 57.1%; Pred. No. 4.2;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 CYDGASVNDNDETC 15
 DB 327 CYDVRTTNEPTCE 340

RESULT 5

Q98977 PRELIMINARY; PRT; 1614 AA.
 AC Q98977;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Complement component C3-3 (Fragment).
 OS *Oncorhynchus mykiss* (Rainbow trout) (*Salmo gairdneri*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96323260; PubMed=8710907;
 RA Sunyer J.O., Zarkadis I.K., Sahu A., Lambiris J.D.;
 RT "Multiple forms of complement C3 in trout that differ in binding to
 complement activators.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8546-8551(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=20437839; PubMed=10980316;
 RA Zarkadis I.K., Sarras M.R., Styroera G., Sunyer J.O., Lambiris J.D.;
 RT "Cloning and structure of three rainbow trout C3 molecules: a
 plausible explanation for their functional diversity.";
 RL Dev. Comp. Immunol. 25:11-24(2001).
 DR EMBL: U61753; AAC60015.2; -;
 DR HSSP: P01024; 1C3D
 DR InterPro: IPR002890; A2M_N.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; MacroglobulinA2.
 DR InterPro: IPR001134; Neutrin_C.
 DR Pfam: PF00207; A2M_1.
 DR Pfam: PF01835; A2M_N_1.
 DR Pfam: PF01821; ANATO_1.
 DR Pfam: PF01759; NTR_1.
 DR PRINTS: PR00004; ANAPHYLATOXN.
 DR PRODOM: PD003264; Anaphylatoxin_1.
 DR SMART: SM00104; ANATO_1
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.

DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
 FT NON-TER 1
 SQ SEQUENCE 1614 AA; 180714 MW; 0910CE3B73D38F10 CRC64;

Query Match 44.3%; Score 50.5; DB 13; Length 1614;
 Best Local Similarity 57.9%; Pred. No. 15;
 Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 CCYDGASVNDNDETCORA 18
 DB 640 CCMGMRKMLDPTCERRA 658

RESULT 6

Q9N497 PRELIMINARY; PRT; 548 AA.
 ID Q9N497;
 AC Q9N497;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Hypothetical 60.1 kDa protein.
 GN Y110A2AL.2.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Rhabditidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Smith A.;
 RT "The sequence of *C. elegans* cosmid Y110A2AL.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC024746; AAF60400.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 548 AA; 60123 MW; C63EC1D429E74989 CRC64;

Query Match 43.4%; Score 49.5; DB 5; Length 548;
 Best Local Similarity 47.4%; Pred. No. 6.7;
 Matches 9; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

QY 1 CC-----YDGASVNDNDETC 14
 DB 171 CCAKRDVFDGSSNNRNETC 189

RESULT 7

Q65686 PRELIMINARY; PRT; 135 AA.
 ID Q65686;
 AC Q65686;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Hypothetical 15.0 kDa protein.
 OS Beet necrotic yellow vein virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
 OX NCBI_TaxID=31721;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=F2;
RA Bouzouba S., Guilley H., Jonard G., Richards K., Putz C.;
RT "nucleotide sequence analysis of rna-3 and rna-4 of beet necrotic
RT yellow vein virus isolates F2 and g1.";
RL J. Gen. Virol. 66:1553-1564(1985).
DR EMBL: M36896; AAA69656.1; -.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 15027 MW; 79E2231BA5240226 CRC64;

Query Match 42.1%; Score 48; DB 12; Length 135;
Best Local Similarity 57.1%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNNDETC 15
Db 115 CYSQVVLSDCLCE 128

RESULT 8

ID 09DS5 PRELIMINARY; PRT; 282 AA.
AC 09DS5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Hypothetical 32.1 kDa protein.
OS Beet necrotic yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=31721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KAS3, AND KAS2;
RX MEDLINE=20456802; PubMed=11003469;
RA Koenig R., Lennfors B.L.;
RT "Molecular analyses of European A, B and P type sources of Beet
RT necrotic yellow vein virus and detection of the rare P type in
RT Kazakhstan.";
RL Arch. Virol. 145:1561-1570(2000).
DR EMBL: AF197557; AAG37097.1; -.
DR EMBL: AF197554; AAG37090.1; -.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 32111 MW; F8D90D3208FB5C1B CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
Best Local Similarity 57.1%; Pred. No. 5.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNNDETC 15
Db 115 CYSQVVLSDCLCE 128

RESULT 9

ID 09DS4 PRELIMINARY; PRT; 282 AA.
AC 09DS4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Hypothetical 32.1 kDa protein.
OS Beet necrotic yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=31721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F75, AND F72;
RX MEDLINE=20456802; PubMed=11003469;
RA Koenig R., Lennfors B.L.;
RT "Molecular analyses of European A, B and P type sources of Beet
RT necrotic yellow vein virus and detection of the rare P type in
RT Kazakhstan.";
RL Arch. Virol. 145:1561-1570(2000).
DR EMBL: AF197548; AAG37084.1; -.

DR EMBL: AF197546; AAG37078.1; -.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 32053 MW; F8DB465FBC6B5C1B CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
Best Local Similarity 57.1%; Pred. No. 5.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNNDETC 15
Db 115 CYSQVVLSDCLCE 128

RESULT 10

ID 09DS5 PRELIMINARY; PRT; 282 AA.
AC 09DS5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Hypothetical 31.9 kDa protein.
OS Beet necrotic yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=31721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D71;
RX MEDLINE=20456802; PubMed=11003469;
RA Koenig R., Lennfors B.L.;
RT "Molecular analyses of European A, B and P type sources of Beet
RT necrotic yellow vein virus and detection of the rare P type in
RT Kazakhstan.";
RL Arch. Virol. 145:1561-1570(2000).
DR EMBL: AF197544; AAG37076.1; -.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 31939 MW; 3383394A3A739F2D CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
Best Local Similarity 57.1%; Pred. No. 5.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNNDETC 15
Db 115 CYSQVVLSDCLCE 128

RESULT 11

ID 09DS75 PRELIMINARY; PRT; 282 AA.
AC 09DS75;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Hypothetical 32.0 kDa protein.
OS Beet necrotic yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=31721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T12;
RX MEDLINE=20456802; PubMed=11003469;
RA Koenig R., Lennfors B.L.;
RT "Molecular analyses of European A, B and P type sources of Beet
RT necrotic yellow vein virus and detection of the rare P type in
RT Kazakhstan.";
RL Arch. Virol. 145:1561-1570(2000).
DR EMBL: AF197552; AAG37088.1; -.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 32024 MW; A463D478D475CF05 CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
Best Local Similarity 57.1%; Pred. No. 5.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNDDETC 15
 DB 115 CYSQVDSDELCE 128

RESULT 12

ID Q9DS67 PRELIMINARY; PRT: 282 AA.
 AC Q9DS67;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Hypoetical 31.9 kDa protein.
 OS Beet necrotic yellow vein virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
 OX NCBI_TaxID=31721;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N7.
 RX MEDLINE=20456802; PubMed=11003469;
 RA Koenig R., Lennfors B.L.;
 RT "Molecular analyses of European A, B and P type sources of Beet necrotic yellow vein virus and detection of the rare P type in Kazakhstan."
 RL Arch. Virol. 145:1561-1570(2000).
 DR EMBL; AF197559; AAC37099.1; -.
 KW Hypoetical protein.
 SQ SEQUENCE 282 AA; 31948 MW; 58A34878C68131F CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
 Best Local Similarity 57.1%; Pred. No. 5.9;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNDDETC 15
 DB 115 CYSQVDSDELCE 128

RESULT 13

ID Q65670 PRELIMINARY; PRT: 282 AA.
 AC Q65670;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE 31k protein.
 OS Beet necrotic yellow vein virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
 OX NCBI_TaxID=31721;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S;
 RX MEDLINE=97128991; PubMed=8973531;
 RA Saito M., Kiguchi T., Kusume T., Tamada T.;
 RT "Complete nucleotide sequence of the Japanese isolate S of beet necrotic yellow vein virus RNA and comparison with European isolates."
 RL Arch. Virol. 141:2163-2175(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C;
 RX Yu J., Han C., Yang L., Li D., Liu Y.;
 RT "cDNA cloning, sequencing and expression of RNA4 from beet necrotic yellow vein virus."
 RL Acta Microbiol. Sin. 37:7-14(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C;
 RX Li D.;
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D84413; BAA12347.1; -.
 DR EMBL; AJ239199; CAA15427.1; -.
 RN [1]

SQ SEQUENCE 282 AA; 31970 MW; D96AA3B079E063E6 CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
 Best Local Similarity 57.1%; Pred. No. 5.9;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNDDETC 15
 DB 115 CYSQVDSDELCE 128

RESULT 14

ID Q9DDV9 PRELIMINARY; PRT: 1684 AA.
 AC Q9DDV9;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 19, Last annotation update)
 DE Complement component C3-4 (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20437839; PubMed=10980316;
 RA Zaratadis I.K., Sarrias M.R., Stryer G., Sunyer J.O., Lambiris J.D.;
 RT "Cloning and structure of three rainbow trout C3 molecules: a plausible explanation for their functional diversity."
 RL Dev. Comp. Immunol. 25:11-24(2001).
 DR EMBL; AF271080; AAG40610.1; -.
 DR HSSP; P01024; IC3D

DR InterPro; IPR002890; A2M_N
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR001599; MacroglobinA2.
 DR InterPro; IPR001134; Netrin_C.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00207; A2M; 1
 DR Pfam; PF01835; A2M_N; 1
 DR Pfam; PF01821; ANATO; 1
 DR Pfam; PF01759; NTR; 1
 DR ProDom; PD003264; Anaphylatoxin; 1.
 DR SMART; SM00104; ANATO; 1.
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
 FT NON_TER 1
 FT TER 1684
 SQ SEQUENCE 1684 AA; 189500 MW; 903802CMAAE4D20D CRC64;

Query Match 41.7%; Score 47.5; DB 13; Length 1684;
 Best Local Similarity 55.0%; Pred. No. 4.9;
 Matches 11; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

OY 1 CCYDGASVNN--DETCORA 18
 DB 717 CCMQMR-NMILDYTCERRS 735

RESULT 15

ID Q9GTY7 PRELIMINARY; PRT: 227 AA.
 AC Q9GTY7;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Ookinete surface antigen-like protein Pf528.
 OS Plasmodium yoelii nigeriensis.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=31274;
 RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=20520976; PubMed=11071297;
RA Taylor D., Cloonan N., Mann V., Cheng Q., Saul A.;
RT "Sequence diversity in rodent malaria of the Pfs28 ookinete surface
antigen homologs.";
RL Mol. Biochem. Parasitol. 110:429-434(2000).
DR EMBL; AF232055; AAC27295.1; -;
DR InterPro; IPR000561; EGF-like.
DR SMART; SM00181; EGF_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
SQ SEQUENCE 227 AA; 24217 MW; A791B0A4E795017 CRC64;

Query Match 41.2%; Score 47; DB 5; Length 227;
Best Local Similarity 46.7%; Pred. NO. 6.8;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 CYDGASVNNDETCQ 16
| | : | : | | :
| | : | : | | :

Db 46 CIDGYGLKNNTCEK 60

Search completed: May 1, 2003, 22:19:15
Job time : 86 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:08:56 ; Search time 36 Seconds
(without alignments)
74.028 Million cell updates/sec

Title: US-09-651-685A-5
Perfect score: 114
Sequence: 1 CCYDASVNNDETCEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
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12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
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21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	22	AAB74055 Human C5a peptide
2	114	100.0	64	18	AAW07784 Human complement C
3	114	100.0	65	18	AAW07785 Human complement C
4	114	100.0	66	18	AAW07786 Human complement C
5	114	100.0	67	18	AAW07787 Human complement C
6	114	100.0	68	18	AAW07788 Human complement C
7	114	100.0	69	18	AAW07789 Human complement C
8	114	100.0	70	18	AAW07790 Human complement C
9	114	100.0	71	18	AAW07782 Human complement C
10	114	100.0	71	18	AAW07783 Human complement C

11	114	100.0	71	18	AAW07804 Human complement C
12	114	100.0	71	18	AAW07791 Human complement C
13	114	100.0	72	18	AAW07792 Human complement C
14	114	100.0	74	22	AAB74053 Human C5a. Homo s
15	111	97.4	20	22	AAB74111 C-terminal truncat
16	110	96.5	20	22	AAB74110 C-terminal truncat
17	110	96.5	20	22	AAB74112 C-terminal truncat
18	110	96.5	20	22	AAB74113 C-terminal truncat
19	110	96.5	20	22	AAB74114 C-terminal truncat
20	110	96.5	20	22	AAB74116 C-terminal truncat
21	110	96.5	74	22	AAB74119 Variant human C5a.
22	109	95.6	19	22	AAB74097 C-terminal truncat
23	109	95.6	20	22	AAB74120 Human C5a peptide
24	109	95.6	74	8	AAV71666 Human anaphylatoxi
25	109	95.6	74	16	AAV75497 Human C5a protein.
26	109	95.6	74	20	AAW959580 Solid phase sequen
27	109	95.6	74	22	AAE05454 Human C5a anaphyla
28	109	95.6	1675	16	AAV77604 pro-C5 polypeptide
29	108	94.7	20	22	AAB74107 C-terminal truncat
30	108	94.7	20	22	AAB74108 C-terminal truncat
31	106	93.0	20	22	AAB74115 C-terminal truncat
32	105	92.1	18	22	AAB74098 C-terminal truncat
33	105	92.1	19	22	AAB74102 C-terminal truncat
34	102	89.5	20	22	AAB74109 C-terminal truncat
35	101	88.6	17	22	AAB74099 C-terminal truncat
36	98	86.0	20	22	AAB74117 C-terminal truncat
37	96	84.2	16	22	AAB74100 C-terminal truncat
38	96	84.2	18	22	AAB74103 C-terminal truncat
39	94	82.5	74	22	AAE05456 Cow C5a anaphylato
40	94	82.5	74	22	AAB74057 Pig C5a anaphylato
41	93	81.6	74	22	AAE05455 Porcine C5a. Sus
42	93	81.6	74	22	AAB74058 C-terminal truncat
43	91	79.8	15	22	AAB74101 C-terminal truncat
44	89	78.1	17	22	AAB74104 Mouse C5a anaphyla
45	88	77.2	77	22	AAE05458

ALIGNMENTS

RESULT 1
AAB74055 standard; Peptide: 20 AA.
ID AAB74055 standard; Peptide: 20 AA.
AC AAB74055;
XX 16-MAY-2001 (first entry)
XX
DT
XX
DE Human C5a peptide fragment #2.
XX
KW Human; C5a; complement; antibody; bacterial infection; sinusitis;
KW meningitis; respiratory; gastrointestinal; urinary tract infection;
KW wound; anaphylatoxin; sepsis.
XX
OS Homo sapiens.
XX
XX WO200115731-A1.
XX
XX 08-MAR-2001.
XX
XX 31-AUG-2000; 2000MO-US24219.
XX
XX 31-AUG-1999; 99US-0387671.
XX
XX (UNMI) UNIV MICHIGAN.
XX
XX Ward PA, Huber-Lang M, Sarma V,
XX WPI; 2001-226665/23.
XX N-PSDB; AAF75793.
XX
XX Compositions for treating blood-borne and toxin mediated diseases and
XX treatment of sepsis in humans and other animals comprises anti-C5a
PT

PT antibodies generated against C-terminal truncated C5a peptides -
 XX
 PS Claim 8; Page 26; 84pp: English.
 CC The present sequence is a peptide fragment of human complement component
 CC C5a (the full-length sequence is given in AAB74053). The present
 CC invention relates to an antibody specific for the present sequence. The
 CC C5a-antibody can be used in a therapeutic composition, which is useful
 CC for treating a subject suffering from bacterial infection, e.g.
 CC sinusitis, meningitis, respiratory, gastrointestinal or urinary tract
 CC infections or infections in wounds. In addition, the C5a antibody can
 CC be used for treating sepsis. C5a is also known as anaphylatoxin.
 XX
 SQ Sequence 20 AA;
 QY Query Match 100.0%; Score 114; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.5e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 CCYDGASVNNDETCERAR 20
 1 CCYDGASVNNDETCERAR 20
 ||||||||||||||||
 RESULT 2
 AAM07784
 ID AAM07784 standard; protein; 64 AA.
 XX
 AC AAM07784;
 XX
 DT 01-SEP-1997 (first entry)
 XX
 DE Human complement C5a protein derivative analogue 1.
 XX
 KW Human; complement; C5a; derivative; receptor; antagonist; trauma;
 KW treatment; prevention; disease; inflammation; pneumonitis; burn;
 KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
 KW post myocardial; infarction; inflammatory bowel; endotoxemic shock;
 KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
 KW immunosuppressive therapy; blood transfusion; dysfunction;
 KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
 KW
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "wild type Thr replaced by Met"
 FT Misc-difference 27 /note= "wild type Cys replaced by Ser"
 FT Misc-difference 64 /note= "wild type Asn replaced by Cys"
 FT
 XX
 PN WO9639503-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 04-JUN-1996; 96WO-EP02422.
 XX
 PR 05-JUN-1995; 95US-0463377.
 PR 05-JUN-1995; 95US-0462648.
 PR 05-JUN-1995; 95US-0463224.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Schmitz A, Van Heeke G, Van Oostrum J;
 XX
 DR WPI; 1997-043125/04.
 XX
 PT New human complement C5a poly-peptide derivs. - used as C5a receptor
 PT antagonists, partic. for treating C5a-mediated diseases and
 PT inflammatory conditions
 XX

PS Example 3; Page -; 93pp: English.
 XX
 CC The present sequence, the human complement C5a derivative 1-64,
 CC Thrlmet, Cys27Ser, Asn64Cys, is a C5a receptor antagonist which
 CC exhibits no agonist activity. It can be used to treat or prevent
 CC C5a mediated diseases or inflammation, e.g. pneumonitis, adult
 CC respiratory distress syndrome (ARDS), pulmonary inflammation or
 CC injury, post myocardial infarction inflammation, inflammatory bowel
 CC disease, rheumatoid arthritis, psoriasis, endotoxemic shock, sepsis,
 CC severe trauma and burns. It can also be used to treat patients
 CC suffering from transplant rejection, receiving immunosuppressive
 CC therapy or massive blood transfusion, exposed to medical devices
 CC or experiencing pulmonary dysfunction following haemodialysis or
 CC leukopheresis. It can also be used as a prophylactic, particularly
 CC in conditions caused by reperfusion, e.g. reperfusion following
 CC ischaemia, and circulatory contact with medical devices, as well as
 CC to prevent transplant rejection.
 CC Antibodies against the derivative can be used to detect or quantify
 CC the derivative and modify, e.g. neutralise, its activity in vivo.
 CC N.B. Sequence not given in specification, but constructed using the
 CC wild type sequence given on pages 51-52.
 XX
 SQ Sequence 64 AA;
 QY Query Match 100.0%; Score 114; DB 18; Length 64;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 21 CCYDGASVNNDETCERAR 40
 1 CCYDGASVNNDETCERAR 20
 ||||||||||||||||
 21 CCYDGASVNNDETCERAR 40
 ||||||||||||||||
 RESULT 3
 AAM07785
 ID AAM07785 standard; protein; 65 AA.
 XX
 AC AAM07785;
 XX
 DT 01-SEP-1997 (first entry)
 XX
 DE Human complement C5a protein derivative analogue 2.
 XX
 KW Human; complement; C5a; derivative; receptor; antagonist; trauma;
 KW treatment; prevention; disease; inflammation; pneumonitis; burn;
 KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
 KW post myocardial; infarction; inflammatory bowel; endotoxemic shock;
 KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
 KW immunosuppressive therapy; blood transfusion; dysfunction;
 KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
 KW
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "wild type Thr replaced by Met"
 FT Misc-difference 27 /note= "wild type Cys replaced by Ser"
 FT Misc-difference 65 /note= "wild type Ile replaced by Cys"
 FT
 XX
 PN WO9639503-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 04-JUN-1996; 96WO-EP02422.
 XX
 PR 05-JUN-1995; 95US-0463377.
 PR 05-JUN-1995; 95US-0462648.
 PR 05-JUN-1995; 95US-0463224.
 XX
 PA (CIBA) CIBA GEIGY AG.

XX PI Schmitz A, Van Heeke G, Van Oostrum J;
 XX DR WPI: 1997-043125/04.
 XX
 PT New human complement C5a poly-peptide derivs. - used as C5a receptor
 PT antagonists, partic. for treating C5a-mediated diseases and
 PT inflammatory conditions
 XX
 PS Example 3; Page -: 93pp; English.
 XX
 CC The present sequence, the human complement C5a derivative 1-65,
 CC Thrlmet, Cys27Ser, Ile65Cys, is a C5a receptor antagonist which
 CC exhibits no agonist activity. It can be used to treat or prevent
 CC C5a mediated diseases or inflammation, e.g. pneumonia, adult
 CC respiratory distress syndrome (ARDS), pulmonary inflammation or
 CC injury, post myocardial infarction inflammation, inflammatory bowel
 CC disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
 CC severe trauma and burns. It can also be used to treat patients
 CC suffering from transplant rejection, receiving immunosuppressive
 CC therapy or massive blood transfusion, exposed to medical devices
 CC or experiencing pulmonary dysfunction following haemodialysis or
 CC leukopheresis. It can also be used as a prophylactic, particularly
 CC in conditions caused by reperfusion, e.g. reperfusion following
 CC ischaemia, and circulatory contact with medical devices, as well as
 CC to prevent transplant rejection.
 CC Antibodies against the derivative can be used to detect or quantify
 CC the derivative and modify, e.g. neutralise, its activity in vivo.
 CC N.B. Sequence not given in specification, but constructed using the
 CC wild type sequence given on pages 51-52.
 CC
 SO Sequence 65 AA:
 Query Match 100.0%; Score 114; DB 18; Length 65;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCYDGASVNDTCQRRAR 20
 Db 21 CCYDGASVNDTCQRRAR 40
 RESULT 4
 AAM07786
 ID AAM07786 standard; protein; 66 AA.
 XX
 AC AAM07786;
 XX
 DT 01-SEP-1997 (first entry)
 XX
 DE Human complement C5a protein derivative analogue 3.
 XX
 KW Human; complement; C5a; derivative; receptor; antagonist; trauma;
 KW treatment; prevention; disease; inflammation; pneumonia; burn;
 KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
 KW post myocardial; infarction; inflammatory bowel; endotoxic shock;
 KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
 KW immunosuppressive therapy; blood transfusion; dysfunction;
 KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 1
 FT MISC-difference 27 /note- "wild type Thr replaced by Met"
 FT MISC-difference 66 /note- "wild type Cys replaced by Ser"
 FT MISC-difference 66 /note- "wild type Ser replaced by Cys"
 XX
 PN W09639503-A1.
 XX

PD 12-DEC-1996.
 XX
 PF 04-JUN-1996; 96WO-EP02422.
 XX
 PR 05-JUN-1995; 95US-0463377.
 PR 05-JUN-1995; 95US-0462648.
 PR 05-JUN-1995; 95US-0463224.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Schmitz A, Van Heeke G, Van Oostrum J;
 XX
 DR WPI: 1997-043125/04.
 XX
 PT New human complement C5a poly-peptide derivs. - used as C5a receptor
 PT antagonists, partic. for treating C5a-mediated diseases and
 PT inflammatory conditions
 XX
 PS Example 3; Page -: 93pp; English.
 XX
 CC The present sequence, the human complement C5a derivative 1-66,
 CC Thrlmet, Cys27Ser, Ser66Cys, is a C5a receptor antagonist which
 CC exhibits no agonist activity. It can be used to treat or prevent
 CC C5a mediated diseases or inflammation, e.g. pneumonia, adult
 CC respiratory distress syndrome (ARDS), pulmonary inflammation or
 CC injury, post myocardial infarction inflammation, inflammatory bowel
 CC disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
 CC severe trauma and burns. It can also be used to treat patients
 CC suffering from transplant rejection, receiving immunosuppressive
 CC therapy or massive blood transfusion, exposed to medical devices
 CC or experiencing pulmonary dysfunction following haemodialysis or
 CC leukopheresis. It can also be used as a prophylactic, particularly
 CC in conditions caused by reperfusion, e.g. reperfusion following
 CC ischaemia, and circulatory contact with medical devices, as well as
 CC to prevent transplant rejection.
 CC Antibodies against the derivative can be used to detect or quantify
 CC the derivative and modify, e.g. neutralise, its activity in vivo.
 CC N.B. Sequence not given in specification, but constructed using the
 CC wild type sequence given on pages 51-52.
 CC
 SO Sequence 66 AA:
 Query Match 100.0%; Score 114; DB 18; Length 66;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCYDGASVNDTCQRRAR 20
 Db 21 CCYDGASVNDTCQRRAR 40
 RESULT 5
 AAM07787
 ID AAM07787 standard; protein; 67 AA.
 XX
 AC AAM07787;
 XX
 DT 01-SEP-1997 (first entry)
 XX
 DE Human complement C5a protein derivative analogue 4.
 XX
 KW Human; complement; C5a; derivative; receptor; antagonist; trauma;
 KW treatment; prevention; disease; inflammation; pneumonia; burn;
 KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
 KW post myocardial; infarction; inflammatory bowel; endotoxic shock;
 KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
 KW immunosuppressive therapy; blood transfusion; dysfunction;
 KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 XX

```

FT MISC-difference 1
FT /note= "wild type Thr replaced by Met"
FT MISC-difference 27
FT /note= "wild type Cys replaced by Ser"
FT MISC-difference 67
FT /note= "wild type His replaced by Cys"
PN WO9639503-A1.
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP02422.
PF
PR 05-JUN-1995; 95US-0463377.
PR 05-JUN-1995; 95US-0462648.
PR 05-JUN-1995; 95US-0463224.
XX
PA (CIBA ) CIBA GEIGY AG.
PI Schmitz A, Van Heeke G, Van Oostrum J;
DR WPI; 1997-043125/04.
XX
XX New human complement C5a polypeptide derivs. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions
XX
XX Example 3; Page -: 93pp; English.
XX
XX The present sequence, the human complement C5a derivative 1-67,
XX ThrlMet, Cys27Ser, His67Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonitis, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients
XX suffering from transplant rejection, receiving immunosuppressive
XX therapy or massive blood transfusion, exposed to medical devices
XX or experiencing pulmonary dysfunction following haemodialysis or
XX leucopheresis. It can also be used as a prophylactic, particularly
XX in conditions caused by reperfusion, e.g. reperfusion following
XX ischaemia, and circulatory contact with medical devices, as well as
XX to prevent transplant rejection.
XX Antibodies against the derivative can be used to detect or quantify
XX the derivative and modify, e.g. neutralise, its activity in vivo.
XX N.B. Sequence not given in specification, but constructed using the
XX wild type sequence given on pages 51-52.
XX
XX Sequence 67 AA:
XX
XX Query Match 100.0%; Score 114; DB 18; Length 67;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCYDGASVNNDETCEQRAAR 20
Db 21 CCYDGASVNNDETCEQRAAR 40

```

```

KW post myocardial infarction; inflammatory bowel; endotoxic shock;
KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
KW immunosuppressive therapy; blood transfusion; dysfunction;
KW haemodialysis; leucopheresis; prophylaxis; reperfusion.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX MISC-difference 1
XX /note= "wild type Thr replaced by Met"
XX MISC-difference 27
XX /note= "wild type Cys replaced by Ser"
XX MISC-difference 68
XX /note= "wild type Lys replaced by Cys"
PN WO9639503-A1.
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP02422.
PF
PR 05-JUN-1995; 95US-0463377.
PR 05-JUN-1995; 95US-0462648.
PR 05-JUN-1995; 95US-0463224.
XX
PA (CIBA ) CIBA GEIGY AG.
PI Schmitz A, Van Heeke G, Van Oostrum J;
DR WPI; 1997-043125/04.
XX
XX New human complement C5a polypeptide derivs. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions
XX
XX Example 3; Page -: 93pp; English.
XX
XX The present sequence, the human complement C5a derivative 1-68,
XX ThrlMet, Cys27Ser, Lys68Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonitis, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients
XX suffering from transplant rejection, receiving immunosuppressive
XX therapy or massive blood transfusion, exposed to medical devices
XX or experiencing pulmonary dysfunction following haemodialysis or
XX leucopheresis. It can also be used as a prophylactic, particularly
XX in conditions caused by reperfusion, e.g. reperfusion following
XX ischaemia, and circulatory contact with medical devices, as well as
XX to prevent transplant rejection.
XX Antibodies against the derivative can be used to detect or quantify
XX the derivative and modify, e.g. neutralise, its activity in vivo.
XX N.B. Sequence not given in specification, but constructed using the
XX wild type sequence given on pages 51-52.
XX
XX Sequence 68 AA:
XX
XX Query Match 100.0%; Score 114; DB 18; Length 68;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCYDGASVNNDETCEQRAAR 20
Db 21 CCYDGASVNNDETCEQRAAR 40

```

```

RESULT 6
AAW07788 standard; protein; 68 AA.
XX
XX AAW07788;
XX
XX 01-SEP-1997 (first entry)
XX
XX Human; complement C5a protein derivative analogue 5.
XX
XX Human; complement; C5a; derivative; receptor; antagonist; trauma;
XX treatment; prevention; disease; inflammation; pneumonitis; burn;
XX adult respiratory distress syndrome; ARDS; pulmonary; injury;
XX

```

AAW07789;
 01-SEP-1997 (first entry)
 Human complement C5a protein derivative analogue 6.
 Human: complement; C5a: derivative; receptor; antagonist; trauma;
 treatment; prevention; disease; inflammation; pneumonitis; burn;
 adult respiratory distress syndrome; ARDS; pulmonary; injury;
 post myocardial infarction; inflammatory bowel; endotoxic shock;
 rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
 immunosuppressive therapy; blood transfusion; dysfunction;
 haemodialysis; leukopheresis; prophylaxis; reperfusion.
 Homo sapiens.
 Synthetic.
 Key Location/Qualifiers
 FT MISC-difference 1 /note= "wild type Thr replaced by Met"
 FT MISC-difference 27 /note= "wild type Cys replaced by Ser"
 FT MISC-difference 69 /note= "wild type Asp replaced by Cys"
 MO9639503-A1.
 12-DEC-1996. 96MO-EP02422.
 04-JUN-1996; 96MO-EP02422.
 05-JUN-1995; 95US-0463377.
 05-JUN-1995; 95US-0462648.
 05-JUN-1995; 95US-0463224.
 (CIBA) CIBA GEIGY AG.
 Schmitz A, Van Heeke G, Van Oostrum J;
 WPI; 1997-043125/04.
 New human complement C5a polypeptide derivs. - used as C5a receptor
 antagonists, partic. for treating C5a-mediated diseases and
 inflammatory conditions
 Example 3; Page -: 93pp; English.
 The present sequence, the human complement C5a derivative 1-69,
 ThrMet, Cys27Ser, Asp69Cys, is a C5a receptor antagonist which
 exhibits no agonist activity. It can be used to treat or prevent
 C5a mediated diseases or inflammation, e.g. pneumonitis, adult
 respiratory distress syndrome (ARDS), pulmonary inflammation or
 injury, post myocardial infarction inflammation, inflammatory bowel
 disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
 severe trauma and burns. It can also be used to treat patients
 suffering from transplant rejection, receiving immunosuppressive
 therapy or massive blood transfusion, exposed to medical devices
 or experiencing pulmonary dysfunction following haemodialysis or
 leukopheresis. It can also be used as a prophylactic, particularly
 in conditions caused by reperfusion, e.g. reperfusion following
 ischemia, and circulatory contact with medical devices, as well as
 to prevent transplant rejection.
 Antibodies against the derivative can be used to detect or quantify
 the derivative and modify, e.g. neutralise, its activity in vivo.
 N.B. Sequence not given in specification, but constructed using the
 wild type sequence given on pages 51-52.
 Sequence 69 AA;
 Query Match 100.0%; Score 114; DB 18; Length 69;
 Best Local Similarity 100.0%; Pred. No. 1.8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTCGEORAR 20
 DB 21 CCYDGASVNDTCGEORAR 40
 RESULT 8
 AAW07790
 ID AAW07790 standard; protein: 70 AA.
 XX
 AC AAW07790;
 01-SEP-1997 (first entry)
 Human complement C5a protein derivative analogue 7.
 Human: complement; C5a: derivative; receptor; antagonist; trauma;
 treatment; prevention; disease; inflammation; pneumonitis; burn;
 adult respiratory distress syndrome; ARDS; pulmonary; injury;
 post myocardial infarction; inflammatory bowel; endotoxic shock;
 rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
 immunosuppressive therapy; blood transfusion; dysfunction;
 haemodialysis; leukopheresis; prophylaxis; reperfusion.
 Homo sapiens.
 Synthetic.
 Key Location/Qualifiers
 FT MISC-difference 1 /note= "wild type Thr replaced by Met"
 FT MISC-difference 27 /note= "wild type Cys replaced by Ser"
 FT MISC-difference 70 /note= "wild type Met replaced by Cys"
 MO9639503-A1.
 12-DEC-1996.
 04-JUN-1996; 96MO-EP02422.
 05-JUN-1995; 95US-0463377.
 05-JUN-1995; 95US-0462648.
 05-JUN-1995; 95US-0463224.
 (CIBA) CIBA GEIGY AG.
 Schmitz A, Van Heeke G, Van Oostrum J;
 WPI; 1997-043125/04.
 New human complement C5a polypeptide derivs. - used as C5a receptor
 antagonists, partic. for treating C5a-mediated diseases and
 inflammatory conditions
 Example 3; Page -: 93pp; English.
 The present sequence, the human complement C5a derivative 1-70,
 ThrMet, Cys27Ser, Met70Cys, is a C5a receptor antagonist which
 exhibits no agonist activity. It can be used to treat or prevent
 C5a mediated diseases or inflammation, e.g. pneumonitis, adult
 respiratory distress syndrome (ARDS), pulmonary inflammation or
 injury, post myocardial infarction inflammation, inflammatory bowel
 disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
 severe trauma and burns. It can also be used to treat patients
 suffering from transplant rejection, receiving immunosuppressive
 therapy or massive blood transfusion, exposed to medical devices
 or experiencing pulmonary dysfunction following haemodialysis or
 leukopheresis. It can also be used as a prophylactic, particularly
 in conditions caused by reperfusion, e.g. reperfusion following
 ischemia, and circulatory contact with medical devices, as well as
 to prevent transplant rejection.
 Antibodies against the derivative can be used to detect or quantify
 the derivative and modify, e.g. neutralise, its activity in vivo.

CC N.B. Sequence not given in specification, but constructed using the
 CC wild type sequence given on pages 51-52.
 XX
 SQ Sequence 70 AA;
 Query Match 100.0%; Score 114; DB 18; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCYDASVNNDETCEORAR 20
 |||||
 DB 21 CCYDASVNNDETCEORAR 40

RESULT 9
 AAM07782
 ID AAM07782 standard; protein; 71 AA.
 XX
 AC AAM07782;
 XX
 DT 01-SEP-1997 (first entry)
 XX
 DE Human complement C5a protein derivative.
 XX
 KW Human: complement; C5a; derivative; receptor; antagonist; trauma;
 KW treatment; prevention; disease; inflammation; pneumonitis; burn;
 KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
 KW post myocardial infarction; inflammatory bowel; endotoxic shock;
 KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
 KW immunosuppressive therapy; blood transfusion; dysfunction;
 KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
 KW
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "wild type Thr replaced by Gly"
 FT Misc-difference 27 /note= "wild type Cys replaced by Ser"
 FT Misc-difference 71 /note= "wild type Gln replaced by Cys"
 FT
 XX W09639503-A1.
 PN
 PD 12-DEC-1996.
 XX
 PF 04-JUN-1996; 96WO-EP02422.
 XX
 PR 05-JUN-1995; 95US-0463377.
 PR 05-JUN-1995; 95US-0462648.
 PR 05-JUN-1995; 95US-0463224.
 XX
 PA (CIBA) CIBA GEIGY AG.
 PI
 PI Schmitz A, Van Heeke G, Van Oostrum J;
 XX
 DR WPI; 1997-043125/04.
 XX
 PT New human complement C5a poly-peptide derivs. - used as C5a receptor
 PT antagonists, partic. for treating C5a-mediated diseases and
 PT inflammatory conditions
 XX
 PS Claim 11; Page -; 93pp; English.
 XX
 CC The present sequence, the human complement C5a derivative 1-71,
 CC Thirily, Cys27Ser, Gln71Cys, is a C5a receptor antagonist which
 CC exhibits no agonist activity. It can be used to treat or prevent
 CC C5a mediated diseases or inflammation, e.g. pneumonitis, adult
 CC respiratory distress syndrome (ARDS), pulmonary inflammation or
 CC injury, post myocardial infarction inflammation, inflammatory bowel
 CC disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
 CC severe trauma and burns. It can also be used to treat patients

CC suffering from transplant rejection, receiving immunosuppressive
 CC therapy or massive blood transfusion, exposed to medical devices
 CC or experiencing pulmonary dysfunction following haemodialysis or
 CC leukopheresis. It can also be used as a prophylactic, particularly
 CC in conditions caused by reperfusion, e.g. reperfusion following
 CC ischaemia, and circulatory contact with medical devices, as well as
 CC to prevent transplant rejection.
 CC Antibodies against the derivative can be used to detect or quantify
 CC the derivative and modify, e.g. neutralise, its activity in vivo.
 CC N.B. Sequence not given in specification, but constructed using the
 CC wild type sequence given on pages 51-52.
 XX
 SQ Sequence 71 AA;
 Query Match 100.0%; Score 114; DB 18; Length 71;
 Best Local Similarity 100.0%; Pred. No. 1.8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCYDASVNNDETCEORAR 20
 |||||
 DB 21 CCYDASVNNDETCEORAR 40

RESULT 10
 AAM07783
 ID AAM07783 standard; protein; 71 AA.
 XX
 AC AAM07783;
 XX
 DT 01-SEP-1997 (first entry)
 XX
 DE Human complement C5a protein derivative.
 XX
 KW Human: complement; C5a; derivative; receptor; antagonist; trauma;
 KW treatment; prevention; disease; inflammation; pneumonitis; burn;
 KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
 KW post myocardial infarction; inflammatory bowel; endotoxic shock;
 KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
 KW immunosuppressive therapy; blood transfusion; dysfunction;
 KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
 KW
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "wild type Thr replaced by Gly"
 FT Misc-difference 27 /note= "wild type Cys replaced by Ser"
 FT Misc-difference 67 /note= "wild type Cys replaced by Ser"
 FT Misc-difference 71 /note= "wild type His replaced by Phe"
 FT Misc-difference 71 /note= "wild type Gln replaced by Cys"
 FT
 XX W09639503-A1.
 PN
 PD 12-DEC-1996.
 XX
 PF 04-JUN-1996; 96WO-EP02422.
 XX
 PR 05-JUN-1995; 95US-0463377.
 PR 05-JUN-1995; 95US-0462648.
 PR 05-JUN-1995; 95US-0463224.
 XX
 PA (CIBA) CIBA GEIGY AG.
 PI
 PI Schmitz A, Van Heeke G, Van Oostrum J;
 XX
 DR WPI; 1997-043125/04.
 XX
 PT New human complement C5a poly-peptide derivs. - used as C5a receptor
 PT antagonists, partic. for treating C5a-mediated diseases and
 PT inflammatory conditions

XX Claim 12, page -: 93pp: English.

XX The present sequence, the human complement C5a derivative 1-71,

XX Thirily, Cys27Ser, His67Phe, Gln71Cys, is a C5a receptor antagonist

CC which exhibits no agonist activity. It can be used to treat or

CC prevent C5a mediated diseases or inflammation, e.g. pneumonia,

CC adult respiratory distress syndrome (ARDS), pulmonary inflammation

CC or injury, post myocardial infarction inflammation, inflammatory

CC bowel disease, rheumatoid arthritis, psoriasis, endotoxic shock,

CC sepsis, severe trauma and burns. It can also be used to treat

CC patients suffering from transplant rejection, receiving

CC immunosuppressive therapy or massive blood transfusion, exposed to

CC medical devices or experiencing pulmonary dysfunction following

CC haemodialysis or leukopheresis. It can also be used as a

CC prophylactic, particularly in conditions caused by reperfusion,

CC e.g. reperfusion following ischaemia, and circulatory contact with

CC medical devices, as well as to prevent transplant rejection.

CC Antibodies against the derivative can be used to detect or quantify

CC the derivative and modify, e.g. neutralise, its activity in vivo.

CC N.B. Sequence not given in specification, but constructed using the

CC wild type sequence given on pages 51-52.

XX

SQ Sequence 71 AA:

Query Match 100.0%; Score 114; DB 18; Length 71;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTCQRAR 20

21 CCYDGASVNDTCQRAR 40

Db

RESULT 11

AAW07804

ID AAW07804 standard; protein; 71 AA.

XX

AC AAW07804;

XX

DT 01-SEP-1997 (first entry)

XX

DE Human complement C5a protein derivative.

XX

KW Human; complement; C5a; derivative; receptor; antagonist; trauma;

KW treatment; prevention; disease; inflammation; pneumonitis; burn;

KW adult respiratory distress syndrome; ARDS; pulmonary; injury;

KW post myocardial infarction; inflammatory bowel; endotoxic shock;

KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;

KW immunosuppressive therapy; blood transfusion; dysfunction;

KW haemodialysis; leukopheresis; prophylaxis; reperfusion.

XX

OS Homo sapiens.

XX

OS Synthetic.

XX

FT Key Location/Qualifiers

FT MISC-difference 1 /note- "wild type Thr replaced by Met"

FT MISC-difference 27 /note- "wild type Cys replaced by Ser"

FT MISC-difference 67 /note- "wild type His replaced by Phe"

FT MISC-difference 71 /note- "wild type Gln replaced by Cys"

XX

XX W09639503-A1.

XX

PD 12-DEC-1996.

XX

PF 04-JUN-1996; 96WO-EP02422.

XX

PR 05-JUN-1995; 95US-0463377.

XX

PR 05-JUN-1995; 95US-0462648.

PR 05-JUN-1995; 95US-0463224.

XX

XX (CIBA) CIBA GEIGY AG.

XX

PI Schmitz A, Van Heeke G, Van Oostrum J;

XX

XX WPI: 1997-043125/04.

DR

DR N-PSDB; AAT47209.

XX

XX New human complement C5a poly-peptide derivs. - used as C5a receptor

PT antagonists, partic. for treating C5a-mediated diseases and

PT inflammatory conditions

XX

XX Example 3; page -: 93pp: English.

XX

XX The present sequence, the human complement C5a derivative 1-71,

CC Thirly, Cys27Ser, His67Phe, Gln71Cys, is a C5a receptor antagonist

CC which exhibits no agonist activity. It can be used to treat or

CC prevent C5a mediated diseases or inflammation, e.g. pneumonia,

CC adult respiratory distress syndrome (ARDS), pulmonary inflammation

CC or injury, post myocardial infarction inflammation, inflammatory

CC bowel disease, rheumatoid arthritis, psoriasis, endotoxic shock,

CC sepsis, severe trauma and burns. It can also be used to treat

CC patients suffering from transplant rejection, receiving

CC immunosuppressive therapy or massive blood transfusion, exposed to

CC medical devices or experiencing pulmonary dysfunction following

CC haemodialysis or leukopheresis. It can also be used as a

CC prophylactic, particularly in conditions caused by reperfusion,

CC e.g. reperfusion following ischaemia, and circulatory contact with

CC medical devices, as well as to prevent transplant rejection.

CC Antibodies against the derivative can be used to detect or quantify

CC the derivative and modify, e.g. neutralise, its activity in vivo.

CC N.B. Sequence not given in specification, but constructed using the

CC wild type sequence given on pages 51-52.

XX

SQ Sequence 71 AA:

Query Match 100.0%; Score 114; DB 18; Length 71;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTCQRAR 20

21 CCYDGASVNDTCQRAR 40

Db

RESULT 12

AAW07791

ID AAW07791 standard; protein; 71 AA.

XX

AC AAW07791;

XX

DT 01-SEP-1997 (first entry)

XX

DE Human complement C5a protein derivative analogue 8.

XX

KW Human; complement; C5a; derivative; receptor; antagonist; trauma;

KW treatment; prevention; disease; inflammation; pneumonitis; burn;

KW adult respiratory distress syndrome; ARDS; pulmonary; injury;

KW post myocardial infarction; inflammatory bowel; endotoxic shock;

KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;

KW immunosuppressive therapy; blood transfusion; dysfunction;

KW haemodialysis; leukopheresis; prophylaxis; reperfusion.

XX

OS Homo sapiens.

XX

OS Synthetic.

XX

FT Key Location/Qualifiers

FT MISC-difference 1 /note- "wild type Thr replaced by Met"

FT MISC-difference 27 /note- "wild type Cys replaced by Ser"

FT MISC-difference 71 /note- "wild type His replaced by Phe"

XX Human; C5a: complement; antibody; bacterial infection; sinusitis;
 KW meningitis; respiratory; gastrointestinal; urinary tract infection;
 KM wound; anaphylatoxin; sepsis.
 XX

OS Homo sapiens.

PN MO200115731-A1.

PD 08-MAR-2001.

PF 31-AUG-2000; 2000MO-US24219.

PR 31-AUG-1999; 99US-0387671.

XX (UNMI) UNIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

PI WPI: 2001-226665/23.

DR N-PSDB; AAF75791.

XX Compositions for treating blood-borne and toxin mediated diseases and
 PT treatment of sepsis in humans and other animals comprises anti-C5a
 PT antibodies generated against C-terminal truncated C5a peptides -

PS Example 7; Page 26; 84pp; English.

CC The present sequence is human complement component C5a. The present
 CC invention relates to an antibody specific for the present sequence. The
 CC C5a antibody can be used in a therapeutic composition, which is useful
 CC for treating a subject suffering from bacterial infection, e.g.
 CC sinusitis, meningitis, respiratory, gastrointestinal or urinary tract
 CC infections or infections in wounds. In addition, the C5a antibody can
 CC be used for treating sepsis. C5a is also known as anaphylatoxin.

XX Sequence 74 AA;

Query Match 100.0%; Score 114; DB 22; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.9e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTECEORAR 20

DB 21 CCYDGASVNDTECEORAR 40

RESULT 15

AAB74111

ID AAB74111 standard; Peptide: 20 AA.

XX AAB74111;

DT 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #49.

KW C5a: complement; antibody; bacterial infection; sinusitis;
 KW meningitis; respiratory; gastrointestinal; urinary tract infection;
 KW wound; anaphylatoxin; sepsis.

XX Unidentified.

PN MO200115731-A1.

PD 08-MAR-2001.

PF 31-AUG-2000; 2000MO-US24219.

PR 31-AUG-1999; 99US-0387671.

XX (UNMI) UNIV MICHIGAN.

PI Ward PA, Huber-Lang M, Sarma V;

DR WPI: 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and
 PT treatment of sepsis in humans and other animals comprises anti-C5a
 PT antibodies generated against C-terminal truncated C5a peptides -

PS Disclosure; Page 30; 84pp; English.

CC The present sequence is a C-terminal truncated C5a peptide fragment. The
 CC present invention relates to an antibody specific for the present
 CC sequence. The C5a-antibody can be used in a therapeutic composition,
 CC which is useful for treating a subject suffering from bacterial
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
 CC urinary tract infections or infections in wounds. In addition, the C5a
 CC antibody can be used for treating sepsis. C5a is also known as
 CC anaphylatoxin.

XX Sequence 20 AA;

Query Match 97.4%; Score 111; DB 22; Length 20;

Best Local Similarity 95.0%; Pred. No. 1.3e-10;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTECEORAR 20

DB 1 CCYDGATVNDTECEORAR 20

Search completed: May 1, 2003, 22:17:25
 Job time : 36 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:19:22 ; Search time 16 Seconds
(Without alignments) 107.858 Million cell updates/sec

Title: US-09-651-685a-5
Perfect score: 114
Sequence: 1 CCYDASVNNDETCEORAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	114	100.0	20	9	US-09-878-603-5	Sequence 5, Appl
2	114	100.0	74	9	US-09-878-603-3	Sequence 3, Appl
3	111	97.4	20	9	US-09-878-603-68	Sequence 68, Appl
4	110	96.5	20	9	US-09-878-603-67	Sequence 67, Appl
5	110	96.5	20	9	US-09-878-603-69	Sequence 69, Appl
6	110	96.5	20	9	US-09-878-603-70	Sequence 70, Appl
7	110	96.5	20	9	US-09-878-603-71	Sequence 71, Appl
8	110	96.5	20	9	US-09-878-603-73	Sequence 73, Appl
9	109	95.6	19	9	US-09-878-603-54	Sequence 54, Appl
10	109	95.6	73	10	US-09-987-675-3	Sequence 3, Appl
11	109	95.6	1251	10	US-09-987-675-3	Sequence 3, Appl
12	109	95.6	1602	10	US-09-987-675-3	Sequence 3, Appl
13	109	95.6	1602	10	US-09-987-675-3	Sequence 3, Appl
14	108	94.7	20	9	US-09-878-603-64	Sequence 64, Appl
15	108	94.7	20	9	US-09-878-603-65	Sequence 65, Appl
16	106	93.0	20	9	US-09-878-603-72	Sequence 72, Appl
17	105	92.1	18	9	US-09-878-603-55	Sequence 55, Appl
18	105	92.1	19	9	US-09-878-603-59	Sequence 59, Appl
19	102	89.5	20	9	US-09-878-603-66	Sequence 66, Appl

20	101	88.6	17	9	US-09-878-603-56	Sequence 56, Appl
21	98	86.0	20	9	US-09-878-603-74	Sequence 74, Appl
22	96	84.2	16	9	US-09-878-603-57	Sequence 57, Appl
23	96	84.2	18	9	US-09-878-603-60	Sequence 60, Appl
24	94	82.5	74	9	US-09-878-603-7	Sequence 7, Appl
25	93	81.6	74	9	US-09-878-603-8	Sequence 8, Appl
26	91	79.8	15	9	US-09-878-603-58	Sequence 58, Appl
27	89	78.1	17	9	US-09-878-603-61	Sequence 61, Appl
28	85	74.6	354	9	US-10-039-050-2	Sequence 2, Appl
29	84	73.7	77	9	US-09-878-603-1	Sequence 1, Appl
30	83	72.8	16	9	US-09-878-603-62	Sequence 62, Appl
31	77	67.5	15	9	US-09-878-603-63	Sequence 63, Appl
32	51	44.7	20	9	US-09-878-603-2	Sequence 2, Appl
33	42	36.8	233	9	US-09-981-876-137	Sequence 137, Appl
34	42	36.8	233	9	US-09-148-545-137	Sequence 137, Appl
35	42	36.8	241	9	US-09-232-880-114	Sequence 114, Appl
36	42	36.8	241	9	US-10-012-896-114	Sequence 114, Appl
37	42	36.8	241	9	US-09-895-793-114	Sequence 114, Appl
38	42	36.8	241	9	US-09-895-814-114	Sequence 114, Appl
39	42	36.8	241	9	US-09-908-193-44	Sequence 44, Appl
40	42	36.8	241	10	US-09-759-143-114	Sequence 114, Appl
41	42	36.8	241	10	US-09-780-669-114	Sequence 114, Appl
42	42	36.8	241	10	US-09-030-606-114	Sequence 114, Appl
43	42	36.8	241	10	US-09-822-827-114	Sequence 114, Appl
44	42	36.8	241	10	US-09-115-453-114	Sequence 114, Appl
45	42	36.8	263	9	US-10-101-392-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-878-603-5
; Sequence 5, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; PIR REFERENCE: UN-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; PRIOR FILING DATE: 2001-06-11
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-878-603-5

Query Match      100.0%; Score 114; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCYDASVNNDETCEORAR 20
Db      1 CCYDASVNNDETCEORAR 20

RESULT 2
US-09-878-603-3
; Sequence 3, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
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FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 3
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-603-3

Query Match
Best Local Similarity 100.0%; Score 114; DB 9; Length 74;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCORAR 20
DB 21 CCYDGASVNNDETCORAR 40

RESULT 3
US-09-878-603-68
Sequence 68, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czernak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 68
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-68

Query Match
Best Local Similarity 97.4%; Score 111; DB 9; Length 20;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCORAR 20
DB 1 CCYDGATVNNDETCORAR 20

RESULT 4
US-09-878-603-67
Sequence 67, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czernak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
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SEQ ID NO 67
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-67

Query Match
Best Local Similarity 96.5%; Score 110; DB 9; Length 20;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCORAR 20
DB 1 CCYDGASVNNDESCORAR 20

RESULT 5
US-09-878-603-69
Sequence 69, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czernak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 69
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-69

Query Match
Best Local Similarity 95.0%; Score 110; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCORAR 20
DB 1 CCYDGASVNNDETCORAR 20

RESULT 6
US-09-878-603-70
Sequence 70, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czernak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 70
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-70

Query Match 96.5%; Score 110; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
||||| |||||||
DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 7
US-09-878-603-71

Sequence 71, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czermak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 71
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-71

Query Match 96.5%; Score 110; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
||||| |||||||
DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 8
US-09-878-603-73

Sequence 73, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czermak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 73
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-73

Query Match 96.5%; Score 110; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 9e-10;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
||||| |||||||
DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 9
US-09-878-603-54
Sequence 54, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czermak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 54
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-54

Query Match 95.6%; Score 109; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAA 19
||||| |||||||
DB 1 CCYDGASVNNDETCEQRAA 19

RESULT 10
US-09-987-675-3
Sequence 3, Application US/09987675
Patent No. US20020169282A1
GENERAL INFORMATION:
APPLICANT: Canne, Lynne
APPLICANT: Kent, Stephen B.H.
APPLICANT: Simon, Reyna
TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
FILE REFERENCE: GREN-023/01US
CURRENT APPLICATION NUMBER: US/09/987,675
CURRENT FILING DATE: 2001-11-15
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 3
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
US-09-987-675-3

Query Match 95.6%; Score 109; DB 9; Length 73;
Best Local Similarity 95.0%; Pred. No. 4.7e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
||||| |||||||
DB 20 CCYDGASVNNDETCEQRAAR 39

RESULT 11
US-09-987-655-3
; Sequence 3, Application US/09987655
; Patent No. US20020132975A1
; GENERAL INFORMATION:
; APPLICANT: Canne, Lynne
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Simon, Reyna
; TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
; TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
; FILE REFERENCE: GREM-023/0105
; CURRENT APPLICATION NUMBER: US/09/987,655
; PRIOR FILING DATE: 2001-11-15
; PRIOR FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-655-3

Query Match 95.6%; Score 109; DB 10; Length 73;
Best Local Similarity 95.0%; Pred. No. 4.7e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
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DB 20 CCYDGACVNNDETCEQRAAR 39

RESULT 12
US-09-778-927A-58
; Sequence 58, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 58
; LENGTH: 1251
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1251)
; OTHER INFORMATION: xaa = any amino acid, unknown, or other
US-09-778-927A-58

Query Match 95.6%; Score 109; DB 10; Length 1251;
Best Local Similarity 95.0%; Pred. No. 8.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
||||| |||||||||
DB 698 CCYDGACVNNDETCEQRAAR 717

RESULT 13
US-09-778-927A-59
; Sequence 59, Application US/09778927A

; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 59
; LENGTH: 1602
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1602)
; OTHER INFORMATION: xaa = any amino acid, unknown, or other
US-09-778-927A-59

Query Match 95.6%; Score 109; DB 10; Length 1602;
Best Local Similarity 95.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
||||| |||||||||
DB 698 CCYDGACVNNDETCEQRAAR 717

RESULT 14
US-09-878-603-64
; Sequence 64, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Caermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: 0M-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 64
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-64

Query Match 94.7%; Score 108; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
||||| |||||||||
DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 15
US-09-878-603-65
; Sequence 65, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.

; APPLICANT: Huber-Lang, Markus
; APPLICANT: Saima, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-65

Query Match 94.7%; Score 108; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCYDGASVNNDETCEQRAAR 20
DB 1 CCYDGASVNNDETCEQRAAR 20

Search completed: May 1, 2003, 22:24:49
Job time : 16 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:16:47 ; Search time 14 Seconds
(without alignments)
42.033 Million cell updates/sec

Title: US-09-651-685A-5
Perfect score: 114
Sequence: 1 CCYDASVNDTCRORAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCYUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	95.6	73	4	US-09-097-094-3
2	109	95.6	74	1	US-08-463-224-3
3	109	95.6	74	2	US-08-463-377-3
4	109	95.6	74	4	US-09-246-500B-10
5	109	95.6	1676	4	US-08-487-283A-2
6	94	82.5	74	4	US-09-246-500B-12
7	93	81.6	74	4	US-09-246-500B-11
8	88	77.2	77	4	US-09-246-500B-14
9	84	73.7	77	4	US-09-246-500B-13
10	84	73.7	77	4	US-09-246-500B-8
11	55.5	48.7	76	4	US-09-246-500B-6
12	51.5	45.2	77	4	US-09-246-500B-7
13	50.5	44.3	77	4	US-09-246-500B-9
14	48.5	42.5	76	4	US-09-246-500B-1
15	43.5	38.2	1651	1	US-08-447-411-2
16	42	36.8	71	2	US-08-972-008-4
17	42	36.8	71	4	US-09-267-409-4
18	42	36.8	211	3	US-08-808-148-1
19	42	36.8	211	4	US-09-020-956-114
20	42	36.8	211	4	US-09-030-607-114
21	42	36.8	211	4	US-09-605-785-114
22	42	36.8	211	4	US-09-439-313-114
23	42	36.8	211	4	US-09-352-616A-114
24	42	36.8	211	4	US-09-232-149A-114
25	42	36.8	263	2	US-08-972-008-2
26	42	36.8	263	4	US-09-141-027-2
27	41.5	36.4	1333	1	US-08-447-411-76

28	41.5	36.4	1333	2	US-08-662-227-34	Sequence 34, Appl
29	41.5	36.4	1333	2	US-08-017-947-34	Sequence 34, Appl
30	41	36.0	363	2	US-08-483-101-16	Sequence 16, Appl
31	40	35.1	751	2	US-08-836-443-3	Sequence 3, Appl
32	40	35.1	802	4	US-09-632-098-2	Sequence 2, Appl
33	40	35.1	812	4	US-09-632-098-4	Sequence 4, Appl
34	40	35.1	1940	2	US-08-644-271-30	Sequence 30, Appl
35	40	35.1	1940	4	US-09-077-955-34	Sequence 34, Appl
36	40	35.1	4544	1	US-08-469-486-52	Sequence 52, Appl
37	40	35.1	4544	2	US-08-469-658-52	Sequence 52, Appl
38	39.5	34.6	256	4	US-09-325-932A-57	Sequence 57, Appl
39	39	34.2	34	2	US-08-867-087B-64	Sequence 64, Appl
40	39	34.2	57	1	US-07-710-361-12	Sequence 12, Appl
41	39	34.2	217	1	US-07-697-275-2	Sequence 2, Appl
42	39	34.2	288	2	US-08-160-224A-6	Sequence 6, Appl
43	39	34.2	4654	4	US-08-476-515A-84	Sequence 84, Appl
44	39	34.2	4655	4	US-08-652-877-84	Sequence 84, Appl
45	39	34.2	4655	4	US-08-652-877-86	Sequence 86, Appl

ALIGNMENTS

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RESULT 1
US-09-097-094-3
Sequence 3, Application US/09097094
Patent No. 6326468
GENERAL INFORMATION:
APPLICANT: Canne, Lynne
APPLICANT: Kent, Stephen B. H.
TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
FILE REFERENCE: GREN-023/01US
CURRENT APPLICATION NUMBER: US/09/097, 094
CURRENT FILING DATE: 1998-06-12
EARLIER APPLICATION NUMBER: 60/049, 553
EARLIER FILING DATE: 1997-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
US-09-097-094-3

Query Match          95.6%   Score 109;   DB 4;   Length 73;
Best Local Similarity 95.0%   Pred. No. 6.2e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDASVNDTCRORAR 20
DB 20 CCYDASVNDTCRORAR 39

RESULT 2
US-08-463-224-3
Sequence 3, Application US/08463224
Patent No. 5807824
GENERAL INFORMATION:
APPLICANT: van Oostrum, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
NUMBER OF SEQUENCES: 67
SUBSTANTIALLY NO. 5807824agonist Activity
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
```


COMPUTER: Macintosh Celris 610
OPERATING SYSTEM: System 7
SOFTWARE: WordPerfect 3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,283A
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,208
FILING DATE: 02-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seth A. Fidel.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-152.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)776-1790
TELEFAX: (203)772-3655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1676 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: Pro-C5 Polypeptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Haviland, D.L.
AUTHORS: Haviland, J.C.
AUTHORS: Fleischer, D.T.
AUTHORS: Hunt, A.
AUTHORS: Wetsel, R.A.
TITLE: Complete cDNA Sequence of Human
Patent No. 6355245
TITLE: Complement Pro-C5
JOURNAL: Journal of Immunology
VOLUME: 146
PAGES: 362-368
DATE: 1991
US-08-487-283A-2

Query Match 95.6%; Score 109; DB 4; Length 1676;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 698 CCYDGACVNNDETCEORAR 717

RESULT 6
US-09-246-500B-12
Sequence 12, Application US/09246500B
Patent No. 6235494
GENERAL INFORMATION:
APPLICANT: Hugill, Tony E.
TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
FILE REFERENCE: 24730-2204
CURRENT APPLICATION NUMBER: US/09/246,500B
CURRENT FILING DATE: 1999-02-08
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 12
LENGTH: 74
TYPE: PRT
ORGANISM: Cow C5a Anaphylatoxin
US-09-246-500B-12

Query Match 82.5%; Score 94; DB 4; Length 74;

Best Local Similarity 80.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 21 CCYDGARVNNDETCEORAR 40

RESULT 7
US-09-246-500B-11
Sequence 11, Application US/09246500B
Patent No. 6235494
GENERAL INFORMATION:
APPLICANT: Hugill, Tony E.
TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
FILE REFERENCE: 24730-2204
CURRENT APPLICATION NUMBER: US/09/246,500B
CURRENT FILING DATE: 1999-02-08
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 11
LENGTH: 74
TYPE: PRT
ORGANISM: Pig C5a Anaphylatoxin
NAME/KEY: CARBOHYD
LOCATION: (64)...(66)
US-09-246-500B-11

Query Match 81.6%; Score 93; DB 4; Length 74;
Best Local Similarity 80.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 21 CCYDGARVNNDETCEORAR 40

RESULT 8
US-09-246-500B-14
Sequence 14, Application US/09246500B
Patent No. 6235494
GENERAL INFORMATION:
APPLICANT: Hugill, Tony E.
TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
FILE REFERENCE: 24730-2204
CURRENT APPLICATION NUMBER: US/09/246,500B
CURRENT FILING DATE: 1999-02-08
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 14
LENGTH: 77
TYPE: PRT
ORGANISM: Mouse C5a Anaphylatoxin
US-09-246-500B-14

Query Match 77.2%; Score 88; DB 4; Length 77;
Best Local Similarity 80.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 24 CCYDGARVNNDETCEORAR 43

RESULT 9
US-09-246-500B-13
Sequence 13, Application US/09246500B
Patent No. 6235494

```
;; GENERAL INFORMATION:
;; APPLICANT: Hugli, Tony E.
;; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
;; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
;; FILE REFERENCE: 24730-2204
;; CURRENT APPLICATION NUMBER: US/09/246,500B
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 13
;; LENGTH: 77
;; TYPE: PRT
;; ORGANISM: Rat C5a Anaphylatoxin
;; FEATURE:
;; NAME/KEY: CARBOHYD
;; LOCATION: (67)...(69)
US-09-246-500B-13
```

```
Query Match          73.7%; Score 84; DB 4; Length 77;
Best Local Similarity 75.0%; Pred. No. 4,4e-06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      1 CCYDASVNDTECEORAR 20
        ||||| | ||||| |
Db      24 CCYDGAENKYECEORVAR 43
```

```
RESULT 10
US-09-246-500B-8
; Sequence 8, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Rat C4a Anaphylatoxin
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (66)...(68)
US-09-246-500B-8
```

```
Query Match          48.7%; Score 55.5; DB 4; Length 76;
Best Local Similarity 57.1%; Pred. No. 0.099;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;
```

```
OY      1 CCYDGS-ASVNDTECEORAR 20
        || | | : ||||| |
Db      23 CCQDGMTRLPMTARCEORAR 43
```

```
RESULT 11
US-09-246-500B-6
; Sequence 6, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
```

```
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 6
;; LENGTH: 77
;; TYPE: PRT
;; ORGANISM: Human C4a Anaphylatoxin
US-09-246-500B-6
```

```
Query Match          45.2%; Score 51.5; DB 4; Length 77;
Best Local Similarity 52.4%; Pred. No. 0.41;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
```

```
OY      1 CCYDGS-VNNDTECEORAR 20
        || | | : ||||| |
Db      23 CCQDGMTRLPMTARCEORAR 43
```

```
RESULT 12
US-09-246-500B-7
; Sequence 7, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Cow C4a Anaphylatoxin
US-09-246-500B-7
```

```
Query Match          44.3%; Score 50.5; DB 4; Length 77;
Best Local Similarity 52.4%; Pred. No. 0.59;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
```

```
OY      1 CCYDGS-VNNDTECEORAR 20
        || | | : ||||| |
Db      23 CCQDGMTRLPMTARCEORAR 43
```

```
RESULT 13
US-09-246-500B-9
; Sequence 9, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 9
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Mouse C4a Anaphylatoxin
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (66)...(68)
US-09-246-500B-9
```

```
Query Match          42.5%; Score 48.5; DB 4; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.2;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
```

```
OY      1 CCYDGS-VNNDTECEORAR 19
```

Db 23 CCODGVTBRLPKRSCQRAA 42

RESULT 14
US-08-447-411-2

Sequence 2, Application US/08447411

Patent No. 5773243

GENERAL INFORMATION:

APPLICANT: FRITZINGER, DAVID C.

APPLICANT: BREDEHORST, REINHARD

APPLICANT: VOGEL, CARL-WILHELM

TITLE OF INVENTION: DNA ENCODING COBRA C3, CWF1, AND CWF2

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/447,411

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/043,747

FILING DATE: 07-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NO. 5773243man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 1126-101-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1651 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-447-411-2

QY 1 CCYDGSVNVNDETCQRA 18

Db 683 CCEDGMHNPMTYCEKRA 701

RESULT 15

US-08-972-008-4

Sequence 4, Application US/08972008

Patent No. 5942420

GENERAL INFORMATION:

APPLICANT: HOLTZMAN, Douglas A.

TITLE OF INVENTION: No. 5942420el Molecules of the Follistatin-Related

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/972,008

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-026

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 71 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-972-008-4

QY 1 CCYDGSVNVNDETCQRAAR 20

Db 39 CGSDGATYRDE--CELRAAR 56

Search completed: May 1, 2003, 22:20:26

Job time: 15 secs

Query Match 36.8%; Score 42; DB 2; Length 71;

Best Local Similarity 50.0%; Pred. No. 11;

Matches 10; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 1, 2003, 22:24:32 ; Search time 15 Seconds
(without alignments)
128.179 Million cell updates/sec

Title: US-09-651-685a-5
Perfect score: 114
Sequence: 1 CCYDASVNDTCQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31.5	27.6	16	2	A59042
2	29.5	25.9	18	1	A58589
3	28	24.6	20	2	B4907
4	26	22.8	13	1	NTKMS
5	25	21.9	16	2	A59045
6	25	21.9	16	2	A54877
7	25	21.9	18	1	QHEC2
8	25	21.9	20	2	PC2248
9	24	21.1	14	2	A48389
10	24	21.1	16	2	PD0002
11	23	20.2	12	2	S28215
12	23	20.2	14	1	NTKIM
13	23	20.2	16	2	PH1317
14	23	20.2	17	2	S60171
15	23	20.2	18	2	D49570
16	23	20.2	18	2	B48839
17	23	20.2	19	2	PS0236
18	23	20.2	20	2	PC1150
19	22	19.3	12	1	A53709
20	22	19.3	13	2	A60379
21	22	19.3	19	2	PH1330
22	22	19.3	20	2	S08605
23	22	19.3	20	2	H49164
24	22	19.3	20	2	A1516
25	21.5	18.9	13	2	B58533
26	21	18.4	10	2	PC4442
27	21	18.4	11	2	D45900
28	21	18.4	15	2	S49409
29	21	18.4	15	2	PH1318

30	21	18.4	16	2	C59045
31	21	18.4	16	2	B54877
32	21	18.4	16	2	H49039
33	21	18.4	16	2	PL0137
34	21	18.4	16	4	I79565
35	21	18.4	17	2	I58087
36	21	18.4	18	2	JT0125
37	21	18.4	19	2	C21182
38	21	18.4	19	2	A21182
39	21	18.4	19	2	A49254
40	21	18.4	19	2	S65435
41	21	18.4	20	2	JT0410
42	21	18.4	20	2	D25507
43	21	18.4	20	2	S48746
44	20	17.5	8	2	D61512
45	20	17.5	11	2	S65395

ALIGNMENTS

RESULT 1
A59042
alpha-conotoxin Epi - cone shell (Conus episcopatus)
C:Species: Conus episcopatus (bishop's cone)
C:Date: 23-Jul-1999 #sequence #revision 23-Jul-1999 #text_change 13-Aug-1999
C:Accession: A59042
R: Loughman, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, J. Biol. Chem. 273, 15667-15674, 1998
A:Title: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopatus that se
A:Reference number: A59042; MUID:98288307; PMID:9624161
A:Accession: A59042
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-16 <CD>
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
F:1-16/Product: alpha-conotoxin Epi #status experimental <MAT>
F:2-8,3-16/Disulfide bonds: #status experimental
F:15/Binding site: sulfated (Tyr) (covalent) #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 27.6%; Score 31.5; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
QY 1 CCYD-GASVNDTC 14
Db 2 CCSDPRCMMNPDYC 16

RESULT 2
A58589
alpha-conotoxin Epi - cone shell (Conus ermineus)
C:Species: Conus ermineus (ermine cone)
C:Date: 10-Sep-1999 #sequence #revision 10-Sep-1999 #text_change 10-Sep-1999
R: Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N
Biochemistry 34, 14519-14526, 1995
A:Title: alpha-Conotoxin Epi, a new nicotinic acetylcholine receptor antagonist with n
A:Reference number: A58589; MUID:96062516; PMID:7578057
A:Accession: A58589
A:Molecule type: protein
A:Residues: 1-18 <MAR>
A:Note: sequence confirmed by chemical synthesis
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline;
F:4-10,5-18/Disulfide bonds: #status experimental
F:18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match

25.9%; Score 29.5; DB 1; Length 18;

Best Local Similarity 33.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 CCYDGSVNNDTC 14
||| : : : |
Db 4 CCHPACGKMPDTC 18

RESULT 3

B44907

manganese peroxidase (EC 1.11.1.13) H3 - basidiomycete (Phanerochaete chrysosporium) (fr
C:Species: Phanerochaete chrysosporium
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 06-Dec-1996
C:Accession: B44907

R:Pease, E.A.; Tien, M.
J. Bacteriol. 174, 3532-3540, 1992

A:Title: Heterogeneity and regulation of manganese peroxidases from Phanerochaete chrysosporium

A:Reference number: A44907; MUID:92276331; PMID:1592808

A:Accession: B44907

A:Molecule type: protein

A:Residues: 1-20 <PEA>

A:Experimental source: BKM-F-1767, ATCC 24725

A:Note: sequence extracted from NCBI backbone (NCBI:104607)

C:Superfamily: lignin peroxidase

C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase

Query Match 24.6%; Score 28; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 7.3e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 DGASVNN 10
||| : : : |
Db 5 DGRKVN 11

RESULT 4

NTRNAS

alpha-conotoxin SIA - cone shell (Conus striatus)

C:Species: Conus striatus (striated cone)

C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-May-1997

C:Accession: A40312

R:Myers, R.A.; Zafaralla, G.C.; Gray, W.R.; Abbott, J.; Cruz, L.J.; Olivera, B.M.
Biochemistry 30, 9370-9377, 1991

A:Title: alpha-Conotoxins, small peptide probes of nicotinic acetylcholine receptors.

A:Reference number: A40312; MUID:91369955; PMID:1892838

A:Accession: A40312

A:Molecule type: protein

A:Residues: 1-13 <MYE>

C:Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot

F:2-7,3-13/Disulfide bonds: #status experimental

F:13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 22.8%; Score 26; DB 1; Length 13;
Best Local Similarity 36.4%; Pred. No. 9.8e+02;

Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCYDGSVNND 11
||| : : : |
Db 2 CCHPACGKMPD 12

RESULT 5

A59045

alpha-conotoxin AUIA - cone shell (Conus aulicus)

C:Species: Conus aulicus (cone cone)

C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C:Accession: A59045

R:Luo, S.; Tjalk, J.M.; Gattler, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McIntosh, J.; Neurosci. 18, 8571-8579, 1998

A:Title: Alpha-conotoxin AUIA selectively blocks alpha3beta4 nicotinic acetylcholine rec

A:Reference number: A59045; MUID:99003392; PMID:9786965

A:Accession: A59045

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <LUO>

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:1-16/Product: alpha-conotoxin AUIA #status experimental <MAT>

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 21.9%; Score 25; DB 2; Length 16;
Best Local Similarity 28.6%; Pred. No. 1.7e+03;

Matches 4; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCYDGSVNNDTC 14
||| : : : |
Db 3 CSTPCCRATNSDYC 16

RESULT 6

A54877

alpha-conotoxin PNIA [validated] - cone shell (Conus pennaceus)

N:Alternate names: alpha-CTX-PNIA

C:Species: Conus pennaceus

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000

C:Accession: A54877

R:Palznicker, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zil

Biochemistry 33, 9523-9529, 1994

A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine r

A:Reference number: A54877; MUID:94347719; PMID:8068627

A:Accession: A54877

A:Molecule type: protein

A:Residues: 1-16 <FAI>

R:Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.

submitted to the Brookhaven Protein Data Bank, January 1996

A:Reference number: A66355; PDB:1PEN

A:Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 21.9%; Score 25; DB 2; Length 16;
Best Local Similarity 28.6%; Pred. No. 1.7e+03;

Matches 4; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCYDGSVNNDTC 14
||| : : : |
Db 3 CSTPCCRATNSDYC 16

RESULT 7

QHEC2

heat-stable enterotoxin ST-2 - Escherichia coli

C:Species: Escherichia coli

C:Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 31-Dec-1996

C:Accession: A01823

R:Chan, S.K.; Giannelis, R.A.

J. Biol. Chem. 256, 7744-7746, 1981

A:Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli

A:Reference number: A01823; MUID:81264141; PMID:7021541

A:Accession: A01823

A:Molecule type: protein

A:Residues: 1-18 <CHA>

A:Experimental source: strain 18D, serotype 0.42:H6:H37

C:Comment: This enterotoxin is one of several, of differing molecular sizes, produced

lines of the heat-stable enterotoxin ST-1.

C:Superfamily: heat-stable enterotoxin ST

C:Keywords: enterotoxin; heat-stable protein

F:1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>

F:5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 21.9%; Score 25; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCY 3
 |||
 DB 9 CCY 11

RESULT 8

PC2248
 Lambda 112 protein - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Sep-1997
 C:Accession: PC2248
 R:Sakai, N.; Inui, K.; Fujii, N.; Fukushima, H.; Nishimoto, J.; Yanagihara, I.; Isegawa, A.;
 Biochem. Biophys. Res. Commun. 198, 485-491, 1994
 A:Title: Krabbe disease: Isolation and characterization of a full-length cDNA for human
 A:Reference number: J02397; MUID:94128088; PMID:8297359
 A:Accession: PC2248
 A:Molecule type: mRNA
 A:Residues: 1-20 <SAK>
 A:Cross-references: DDBJ:D25284

Query Match 21.9%; Score 25; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCY 3
 |||
 DB 5 CCY 7

RESULT 9

A48389
 Lelutrotoxin III - Egyptian scorpion (fragment)

C:Species: Lelurus quingestratus (Egyptian scorpion)
 C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
 C:Accession: A48389
 R:Valdavid, H.H.; Martin, B.M.; Escobar, L.; Possani, L.D.
 Biochem. Int. 27, 953-962, 1992
 A:Title: Noxiustoxin and lelutrotoxin III, two homologous peptide toxins with binding pro
 A:Reference number: A48389; MUID:93075256; PMID:1280139
 A:Accession: A48389
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <VAL>
 A:Experimental source: venom
 A:Note: sequence extracted from NCBI backbone (NCBIP:117118)

Query Match 21.1%; Score 24; DB 2; Length 14;
 Best Local Similarity 35.7%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

OY 2 CYDGASVNDDET 15
 |||
 DB 7 CYDSSQ-----CE 14

RESULT 10

PD0002
 Inulin fructotransferase (depolymerizing, difructofuranose-1,2'-2,3'-dianhydride-forming

C:Species: Bacillus sp.
 C:Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 03-Jun-2002
 C:Accession: PD0002
 R:Kang, S.I.; Kim, W.P.; Chang, Y.J.; Kim, S.I.
 Biosci. Biotechnol. Biochem. 62, 628-631, 1998
 A:Title: Purification and properties of inulin fructotransferase (DFA III-producing) fr
 A:Reference number: PD0002
 A:Accession: PD0002
 A:Molecule type: protein
 A:Residues: 1-16 <KAN>
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 21.1%; Score 24; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 DGASVNDDET 13
 |||
 DB 5 DGAPLVQVNT 14

RESULT 11

S28215
 glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) GII - barley (fragment)

N:Alternate names: (1-3)-beta-D-glucanase GII
 C:Species: Hordeum vulgare (barley)
 C:Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 07-May-1999
 C:Accession: S28215
 R:Hrmova, M.; Fincher, G.B.
 Biochem. J. 289, 453-461, 1993
 A:Title: Purification and properties of three (1->3)-beta-D-glucanase isoenzymes from
 A:Reference number: S28214; MUID:93143715; PMID:8424790
 A:Accession: S28215
 A:Molecule type: protein
 A:Residues: 1-12 <HRM>
 A:Experimental source: cultivar Clipper
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 20.2%; Score 23; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.6e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CYDGASVN 9
 |||
 DB 4 CYGGIGNN 11

RESULT 12

NTKNIIM
 alpha-conotoxin MI - cone shell (Conus magus)

C:Species: Conus magus (magus cone)
 C:Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 16-Jul-1999
 C:Accession: A01784
 R:McIntosh, M.; Cruz, L.J.; Hunkapiller, M.W.; Gray, W.R.; Olivera, B.M.
 Arch. Biochem. Biophys. 218, 329-334, 1982
 A:Title: Isolation and structure of a peptide toxin from the marine snail Conus magus
 A:Reference number: A90071; MUID:83073458; PMID:7149738
 A:Accession: A01784
 A:Molecule type: protein
 A:Residues: 1-14 <MC1>
 R:Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.
 J. Biol. Chem. 258, 12247-12251, 1983
 A:Title: Conotoxin MI. Disulfide bonding and conformational states.
 A:Reference number: A92396; MUID:84032400; PMID:6630187
 A:Contents: annotation; disulfide bonds
 C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn
 C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
 E:3-8,4-14/Disulfide bonds: #status experimental
 E:14/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 20.2%; Score 23; DB 1; Length 14;
 Best Local Similarity 33.3%; Pred. No. 3e+03;
 Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CCYDGASVN 9
 |||
 DB 3 CCHPACGKN 11

RESULT 13

PH1317
 Ig heavy chain DJ region (clone C527-112) - human (fragment)
 C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1317
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A>Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MIMD:93094761; PMID:1460419
A:Accession: PH1317
A:Molecule type: DNA
A:Residues: 1-16 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 20.2%; Score 23; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 CYDGAS 7
|||:
Db 5 CYGGS 10

RESULT 14

S60171
sex-lethal protein - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 17-Mar-1999
C:Accession: S60171
R:Hoshijima, K.; Kohyama, A.; Watakabe, I.; Inoue, K.; Sakamoto, H.; Shimura, Y.
Nucleic Acids Res. 23, 3441-3448, 1995
A>Title: Transcriptional regulation of the Sex-lethal gene by helix-loop-helix proteins.
A:Reference number: S60171; MIMD:96032836; PMID:7567454
A:Accession: S60171
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-17 <HOS>
A:Cross-references: EMBL:D50435
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C:Genetics:
A:Gene: FlyBase:Sxl
A:Cross-references: FlyBase:FBgn0003659

Query Match 20.2%; Score 23; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 3.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 13 TCEORA 18
|||:
Db 12 TCYORS 17

RESULT 15

D49570
plasma membrane calcium pump - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 12-Dec-1997
C:Accession: D49570
R:Stautfer, T.P.; Hilfinger, H.; Carafoli, E.; Strehler, E.E.
J. Biol. Chem. 268, 25993-26003, 1993
A>Title: Quantitative analysis of alternative splicing options of human plasma membrane
A:Reference number: A49570; MIMD:94064681; PMID:8245032
A:Accession: D49570
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-18 <STRA>
A:Experimental source: cerebral cortex
A>Note: sequence inconsistent with nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:139934, NCBIP:139939)
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP

Query Match 20.2%; Score 23; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 CYDG 5
|||:
Db 5 CWDG 8

Search completed: May 1, 2003, 22:27:40
Job time : 17 secs

GenCore version 5.1.4-p5.4578
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OW protein - protein search, using sw model

Run on: May 1, 2003, 22:20:32 ; Search time 25 Seconds

(without alignments)
33.181 Million cell updates/sec

Title: US-09-651-685a-5

Sequence: 1 CCYDGSVNNDETCGRRAR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1147

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.5	27.6	16	1	CXAL_CONEP
2	29.5	25.9	18	1	CXAL_CONEP
3	29	25.4	15	1	ITRB_ALBU
4	26	22.8	13	1	CXAA_CONST
5	25	21.9	16	1	CXAL_CONEP
6	25	21.9	16	1	CXAA_CONEP
7	25	21.9	18	1	HSTB_ECOLI
8	25	21.9	19	1	LCRP_PETMA
9	24	21.1	14	1	SCK3_LEIOU
10	24	20.2	20	1	SB60_MAIZE
11	23	20.2	14	1	CXAL_CONEP
12	22	19.3	12	1	CXAL_CONEP
13	21	18.4	15	1	UNO1_PINPS
14	21	18.4	16	1	CXAB_CONEP
15	21	18.4	18	1	PMW2_LIMPO
16	21	18.4	18	1	PMW2_LIMPO
17	21	18.4	20	1	SC18_MESMA
18	20	17.5	10	1	RRLP_PHOVY
19	20	17.5	11	1	CX5A_CONEP
20	20	17.5	11	1	CX5B_CONEP
21	20	17.5	13	1	CX1A_CONEP
22	20	17.5	14	1	CX1A_CONEP
23	20	17.5	14	1	CX1B_CONEP
24	20	17.5	15	1	CX1B_CONEP
25	20	17.5	15	1	OBPA_MAMBR
26	20	17.5	15	1	TERM_BP2
27	20	17.5	16	1	FOR1_MYRGU
28	20	17.5	17	1	TAC3_TACGI
29	20	17.5	17	1	TAC3_TACGI
30	20	17.5	18	1	PPM1_LIMPO
31	20	17.5	19	1	H170_RAT
32	19	16.7	9	1	OXYA_SCYCA
33	19	16.7	9	1	OXYA_SQUAC

34	19	16.7	10	1	COXA_ONCMY
35	19	16.7	10	1	PPCK_FASHE
36	19	16.7	10	1	UH05_RAT
37	19	16.7	15	1	GUAN_DIDMA
38	19	16.7	16	1	ARCD_PSEPU
39	19	16.7	17	1	CXMA_CONEP
40	19	16.7	17	1	CXMA_CONEP
41	19	16.7	17	1	PATS_ANASP
42	19	16.7	18	1	RL24_PROVU
43	19	16.7	18	1	UC03_MAIZE
44	19	16.7	19	1	FLTB_TAPTE
45	19	16.7	19	1	HMD_METWO

ALIGNMENTS

RESULT 1	
CXAL_CONEP	STANDARD; PRT; 16 AA.
ID	P5638;
AC	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DE	15-JUN-2002 (Rel. 41, Last annotation update)
OS	Alpha-conotoxin Epi.
OC	Conus episcopatus (Bishop's cone).
NC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
NC	Neogastropoda; Conoidea; Conidae; Conus.
NC	NCBI_TaxID=88764;
RA	X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RA	MEDLINE=98376423; PubMed=9708977;
RA	Hu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,
RT	Alewood P.F., Lewis R.J., Martin J.L.;
RT	"The 1.1-A resolution crystal structure of [Tyr15]Epi, a novel
RT	alpha-conotoxin from Conus episcopatus, solved by direct methods."
RT	Biochemistry 37:11425-11433(1998).
CC	-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC	BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC	INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC	ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 AND ALPHA-
CC	3/BETA-4 SUBUNITS.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC	-1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
DR	PDB: 1A0M, 13-JAN-99.
KW	postsynaptic neurotoxin; Neurotoxin; Toxin;
KW	Acetylcholine receptor inhibitor; Amlidation;
FT	Disulfid; 3D-structure.
FT	DISULFID 2
FT	MOD.RES 3 16
FT	MOD.RES 15 15
FT	MOD.RES 16 16
SO	SEQUENCE 16 AA; 1792 MW; C63385F37C99B4C CRC64;
	SULFATION.
	AMIDATION.
	Query Match 27.6%; Score 31.5; DB 1; Length 16;
	Best local Similarity 40.0%; Pred.No.48;
	Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
OY	1 CCYD-GASVNNDETC 14
DB	2 CCSDPRCNNNDPYC 16
RESULT 2	
CXAL_CONEP	STANDARD; PRT; 18 AA.
ID	P50982;
AC	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Alpha-conotoxin E1.

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OS Conus ermineus (Atlantic fish-hunting cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=55423;

RN
RP SEQUENCE.
RC MEDLINE=96062516; PubMed=7578057;
RX Martinez J.S., Olivera B.M., Gray W.R., Craig A.G., Groebe D.R.,
RA Abramson S.N., McIntosh J.M.;
RT "Alpha-conotoxin EI, a new nicotinic acetylcholine receptor
antagonist with novel selectivity."
RL Biochemistry 34:14519-14526(1995).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC -1- SUBUNIT: Binds nicotinic acetylcholine receptor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
CC Postsynaptic neurotoxin; Neurotoxin; Toxin;
KM Acetylcholine receptor inhibitor; Amidation; Hydroxylation.
FT DISULFID 4 10
FT DISULFID 5 18
FT MOD_RES 3 3 HYDROXYLATION.
FT MOD_RES 18 18 AMIDATION.
SQ SEQUENCE 18 AA; 2082 MW; 60A61AC427A6B5E CRC64;

Query Match 25.9%; Score 29.5; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

OY 1 CCYDGSVNNDEC 14
DB 4 CCYHPTCMSNPQIC 18

RESULT 3
ITRB ALBU
ID ITRB ALBU STANDARD; PRT; 15 AA.
AC P24927;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Trypsin inhibitor B chain (Fragment).
DE Albizzia julibrissin (Silk tree).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Mimosoideae; Ingeae; Albizia.
OX NCBI_TaxID=3813;
RN [1]
RP SEQUENCE.
RC MEDLINE=80115605; PubMed=528539;
RX Odani S., Ono T., Ikenaka T.;
RT "Proteinase inhibitors from a mimosoideae legume, Albizzia
julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";
RL J. Biochem. 86:1795-1805(1979).
CC -1- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.
CC -1- SUBUNIT: HETERODIMER OF AN "A" AND A "B" CHAIN LINKED BY A
CC DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE LEGUMINOS KUNITZ-TYPE INHIBITOR
CC FAMILY.
CC Serine protease inhibitor.
KM NON_TER 15
FT SEQUENCE 15 AA; 1705 MW; 53165F7E9C45B4D0 CRC64;

Query Match 25.4%; Score 29; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 CYDGSVNNDE 12

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DB 5 CKDGSIDDE 15

RESULT 4
CXAL CONST
ID CXAL CONST STANDARD; PRT; 13 AA.
AC P28678;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin SIA (SIA).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
CC PIR: A40312; NTKNAS.
KM Postsynaptic neurotoxin; Neurotoxin; Toxin;
KM Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;

Query Match 22.8%; Score 26; DB 1; Length 13;
Best Local Similarity 36.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 CCYDGSVNNDD 11
DB 2 CCHPACGKNFD 12

RESULT 5
CXAL CONAL
ID CXAL CONAL STANDARD; PRT; 16 AA.
AC P56639;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin AUIA.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99003392; PubMed=9786965;
RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
RA Olivera B.M., McIntosh J.M.;
RT "Alpha-conotoxin AUIB selectively blocks alpha3 beta4 nicotinic
acetylcholine receptors and nicotine-evoked norepinephrine release."
RL J. Neurosci. 18:8571-8579(1998).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC

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CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE FAMILY.
 DR HSP: P50984; 1PEN.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KM Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA: 1731 MW: 1E310FB8FDC7001 CRC64;

Query Match 21.9%; Score 25; DB 1; Length 16;
 Best Local Similarity 28.6%; Pred. No. 5.1e+02;
 Matches 4; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCYDASVNNDETC 14
 DB 3 CSYPCFATNSDYC 16

RESULT 6

ID CXXA_CONPE STANDARD; PRT: 16 AA.
 AC P50984;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Pn1A.
 OS Conus pennaceus (Feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conidae; Conus.
 OX NCBI_TaxID=37335;

RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=94347719; PubMed=8068627;
 RA Fainzilber M., Hesson A., Oren R., Burlingame A.L., Gordon D.,
 RA Spira M.E., Zlotkin E.;
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
 RT acetylcholine receptors.";
 RL Biochemistry 33:9523-9529(1994).
 RN [2]
 RP Sulfation of Tyr-15.
 RX MEDLINE=99242956; PubMed=10226369;
 RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
 RA Baldwin M.A., Burlingame A.L.;
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
 RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
 RT phosphopeptides by electrospray, matrix-assisted laser
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
 RT spectrometry.";
 RL J. Mass Spectrom. 34:447-454(1999).
 RN [3]

RA X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RX MEDLINE=96311277; PubMed=8740364;
 RA Hu S.-H., Gehrmann J., Guedat L.W., Alewood P.F., Craik D.J.,
 RA Martin J.L.;
 RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
 RT antagonist, alpha-conotoxin Pn1A from Conus pennaceus.";
 RL Structure 4:417-423(1996).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES. THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
 CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
 CC PENNACEUS ALPHA-CONOTOXINS SECRETED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PDB: 1PEN; 21-APR-97.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KM Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA: 1628 MW: 03310FF95SEC99005 CRC64;

Query Match 21.9%; Score 25; DB 1; Length 16;
 Best Local Similarity 28.6%; Pred. No. 5.1e+02;
 Matches 4; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 CCYDASVNNDETC 14
 DB 3 CSUPECAANNPDYC 16

RESULT 7

ID HSTR_ECOLI STANDARD; PRT: 18 AA.
 AC P01360;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Heat-stable enterotoxin ST-2 (ST-B).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]

RP SEQUENCE.
 RC STRAIN=042; K86:H37 / 18D.
 RX MEDLINE=8126411; PubMed=7021541;
 RA Chan S.-K., Giannella R.A.;
 RT "Amino acid sequence of heat-stable enterotoxin produced by
 RT Escherichia coli pathogenic for man.";
 RL J. Biol. Chem. 256:7744-7746(1981).
 RN [2]

RP DISULFIDE BONDS.
 RX MEDLINE=87191003; PubMed=3552731;
 RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Almoto S., Takeda T.,
 RA Miwatani T., Takeda Y.;
 RT "Mode of disulfide bond formation of a heat-stable enterotoxin (StH)
 RT produced by a human strain of enterotoxigenic Escherichia coli.";
 RL FEBS Lett. 215:165-170(1987).
 CC -1- FUNCTION: TOXIN WHICH ACTIVATES THE PARTICULATE FORM OF GUANYLATE
 CC CYCLASE AND INCREASES CYCLIC GMP LEVELS WITHIN THE HOST
 CC INTESTINAL EPITHELIAL CELLS.
 CC -1- DISEASE: BOTH HEAT-STABLE AND HEAT-LABILE ENTEROTOXINS ARE
 CC PRODUCED BY PATHOGENIC STRAINS OF E. COLI AND AFFECT THE DIGESTIVE
 CC TRACT OF MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE HEAT-STABLE ENTEROTOXIN FAMILY.
 DR PIR: A01823; OHEC2.
 DR HSP: P01359; IETN.
 DR InterPro: IPR001489; Enterotoxin_HS.
 DR Pfam: PF02048; Enterotoxin_HS; 1.
 DR PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.

KW Toxin; Enterotoxin.
 FT DISULFID 5 10
 FT DISULFID 6 14
 FT DISULFID 9 17
 SQ SEQUENCE 18 AA: 1978 MW: D0C975F49D600650 CRC64;

Query Match 21.9%; Score 25; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCY 3
 DB 9 CCY 11

RESULT 8

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LCRP_PETMA
ID LCRP_PETMA STANDARD: PRT: 19 AA.
AC 010936:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Corticostatin-related protein LCRP.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RC MEDLINE=96321324; PubMed=8759287;
RA Conlon J.M., Sower S.A.
RT "Isolation of a peptide structurally related to mammalian
RT corticostatin from the lamprey Petromyzon marinus.";
RL Comp. Biochem. Physiol. 114B:133-137(1996).
CC -1- FUNCTION: MAY HAVE MICROBICIDAL ACTIVITIES. MAY INHIBIT
CC CORTICOTROPIN (ACTH) STIMULATED STEROIDOGENESIS AND THE MICROBIAL
CC ACTIONS OF THE CORTICOSTATINS.
CC -1- MASS SPECTROMETRY: MW=2201; MW_ERR=0.4; METHOD=Electrospray.
CC DEFENSIN: BELONGS TO THE CORTICOSTATIN/DEFENSIN FAMILY.
KM DEFENSIN: Antibiolic.
FT DISULFID 1 18 BY SIMILARITY.
FT DISULFID 3 9 BY SIMILARITY.
FT DISULFID 8 17 BY SIMILARITY.
SQ SEQUENCE 19 AA: 2209 MW: 8D9CEDC71A199A55 CRC64;

Query Match 21.9%; Score 25; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCYDGASY 8
| | | | |
Db 8 CCVAGLNV 15

RESULT 9
SCK3_LEIUO
ID SCK3_LEIUO STANDARD: PRT: 14 AA.
AC P45661:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Leiturutoxin III (Fragment).
OS Leiturus quinquestratus quinquestratus (Egyptian scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthidae; Butthidae; Leiturus.
OX NCBI_TaxID=6885;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Valdivia H.H., Martin B.M., Escobar L., Possant L.D.;
RA "Noxiustoxin and leiturutoxin III, two homologous peptide toxins with
RA binding properties to synaptosomal membrane K+ channels.";
RL Biochem. Int. 27:953-962(1992).
CC -1- FUNCTION: BLOCKER OF POTASSIUM CHANNELS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CC CHANNEL INHIBITORS SUBFAMILY.
DR InterPro: IPR001947; Scorpion_toxins.
DR PROSITE: PS01138; SCORP_SHORT_TOXIN; PARTIAL.
KW Neurotoxin; Potassium channel inhibitor.
FT NON_TER 14
FT SEQUENCE 14 AA: 1588 MW: 83C67CCBD691205E CRC64;

Query Match 21.1%; Score 24; DB 1; Length 14;
Best Local Similarity 35.7%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

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OY 2 CYDGASVNDTECE 15
| | | | |
Db 7 CYDSSQ-----CE 14

RESULT 10
SB60_MAIZE
ID SB60_MAIZE STANDARD: PRT: 20 AA.
AC P82868:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative 60 kDa spermidine-binding protein (fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RC STRAIN=cv. Cecilia; TISSUE=Coleoptile;
RA Tassoni A., Napier R.M., Franceschetti M., Venis M.A., Bagni N.;
RT "Spermidine-binding proteins: purification and expression analysis in
RT Zea mays.";
RL Plant Physiol. 0:0-0(2002).
CC -1- FUNCTION: May have spermidine-binding activity.
CC -1- SUBUNIT: Dimer of 18 kDa and 60 kDa subunit (Probable).
CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane.
CC -1- MISCELLANEOUS: On the 2D-gel its MW is: 60 kDa.
KW Membrane; Mitosome.
FT NON_TER 20
FT SEQUENCE 20 AA: 2093 MW: 7FD730C00391579A CRC64;

Query Match 21.1%; Score 24; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.1e+02;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 6 ASVNDTECEGRAR 20
| | | | |
Db 4 AVEPPEPSONRIAK 18

RESULT 11
CXAL_CONMA
ID CXAL_CONMA STANDARD: PRT: 14 AA.
AC P01521:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin MI (MI).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE.
RC MEDLINE=83073458; PubMed=7149738;
RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
RA "Isolation and structure of a peptide toxin from the marine snail
RA Conus magus.";
RL Arch. Biochem. Biophys. 218:329-334(1982).
RN [2]
RP DISULFIDE BONDS.
RC MEDLINE=84032400; PubMed=6630187;
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
RA "Conotoxin MI. Disulfide bonding and conformational states.";
RL J. Biol. Chem. 258:12247-12251(1983).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE

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CC FAMILY.
 DR PTR: A01784; NTRK1M.
 DR HSSP; P56973; 1B45.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 FT Acetylcholine receptor inhibitor; Amdaction.
 FT DISULFID 3 8
 FT DISULFID 4 14
 FT MOD.RES 14 14
 SQ SEQUENCE 14 AA; 1499 MW; DEEE91898BFE5BD CRC64;
 MIDACTION.
 Query Match 20.2%; Score 23; DB 1; Length 14;
 Best Local Similarity 33.3%; Pred. No. 9.1e+02;
 Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CCIDGASVN 9
 DB 3 CCHPACGKN 11

RESULT 12
 CXAL_CONIM STANDARD; PRT; 12 AA.
 AC P50983;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Imi.
 OS Conus imperialis (Imperial cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conidae; Conidae; Conus.
 OX NCBI_TaxID=35631;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE-venom.
 RX MEDLINE=94266889; PubMed=8206995;
 RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,
 RA Gray W.R., Oliveira B.M.;
 RT "A nicotinic acetylcholine receptor ligand of unique specificity,
 RL alpha-conotoxin Imi.";
 RL J. Biol. Chem. 269:16733-16739(1994).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=95379776; PubMed=7651351;
 RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
 RA McIntosh J.M.;
 RT "Alpha-conotoxin Imi exhibits subtype-specific nicotinic
 RT acetylcholine receptor blockade: preferential inhibition of homomeric
 alpha 7 and alpha 9 receptors.";
 RL Mol. Pharmacol. 48:194-199(1995).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99212205; PubMed=10194298;
 RA Rogers J.P., Luginduhl P., Shen G.S., McCabe R.T., Stevens R.C.,
 RA Wemmer D.E.;
 RT "NMR solution structure of alpha-conotoxin Imi and comparison to
 RT other conotoxins specific for neuronal nicotinic acetylcholine
 RT receptors.";
 RL Biochemistry 38:3874-3882(1999).
 RN [4]
 RP STRUCTURE BY NMR.
 RX PubMed=10350614;
 RA Gouda H., Hiroto S.;
 RT "Solution structure of alpha-conotoxin Imi determined by
 RT two-dimensional NMR spectroscopy.";
 RL Biochim. Biophys. Acta 1431:384-394(1999).
 RN [5]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99158061; PubMed=10050774;
 RA Maslennikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,
 RA Meltesse C., Tseclin V.I., Arseniev A.S.;
 RT "NMR spatial structure of alpha-conotoxin Imi reveals a common
 RT scaffold in small and snake toxins recognizing neuronal nicotinic
 RT acetylcholine receptors.";

RL FEBS Lett. 444:275-280(1999).
 RN [6]
 RP STRUCTURE BY NMR.
 RX PubMed=10431825;
 RA Lamthanh H., Jegou-Matheron C., Servent D., Menez A., Lancelin J.-M.;
 RT "Minimal conformation of the alpha-conotoxin Imi for the alpha7
 RT neuronal nicotinic acetylcholine receptor recognition: correlated CD,
 RT NMR and binding studies.";
 RL FEBS Lett. 454:293-298(1999).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99324017; PubMed=10395477;
 RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
 RT "Solution structure of alpha-conotoxin Imi by 1H nuclear magnetic
 RT resonance.";
 RL J. Med. Chem. 42:2364-2372(1999).
 RN [8]
 RP MUTAGENESIS OF ASP-5; ARG-7 AND ARG-11, AND STRUCTURE BY NMR OF THESE
 RP THREE MUTANTS.
 RX PubMed=11124036;
 RA Rogers J.P., Luginduhl P., Pemberton K., Hartly P., Wemmer D.E.,
 RA Stevens R.C.;
 RT "Structure-activity relationships in a peptidic alpha7 nicotinic
 RT acetylcholine receptor antagonist.";
 RL J. Mol. Biol. 304:911-926(2000).
 CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
 CC inhibit them. It is highly active against the neuromuscular
 CC receptor in frog but not in mice. In contrast, it induces seizures
 CC when injected centrally in mice and rats. It targets neuronal
 CC nAChRs in mammals. It blocks homomeric alpha-7 nicotinic receptors
 CC with 8-fold lower affinity. It has no effect on receptors composed
 CC of alpha-2/beta-4, or alpha-3/beta-2, alpha-4/beta-2, alpha-2/beta-4,
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PDB: 1IM1; 15-JUN-99.
 DR PDB: 1IMI; 23-APR-99.
 DR PDB: 1CNL; 27-MAY-99.
 DR PDB: 1E74; 27-DEC-00.
 DR PDB: 1E75; 27-DEC-00.
 DR PDB: 1E76; 27-DEC-00.
 DR PDB: 1G2G; 08-NOV-00.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amdaction; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 12
 FT MOD.RES 12 12
 FT MUTAGEN 5 5
 FT MUTAGEN 7 7
 FT MUTAGEN 11 11
 SQ SEQUENCE 12 AA; 1357 MW; 9C29CEA545A1176A CRC64;
 MIDACTION.
 D->L:REDUCTION OF TOXICITY.
 R->E:REDUCTION OF TOXICITY.
 R->E:NO LOSS OF ACTIVITY.

Query Match 19.3%; Score 22; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCYD 4
 DB 2 CCSD 5

RESULT 13
 UNO1_PINPS STANDARD; PRT; 15 AA.
 ID UNO1_PINPS
 AC P81106;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (S1247/S1248) (N150/N151)

DE (Fragment).
 OS Pinus pinaster (Maritime pine).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 NCBI_TaxID=71647;
 RN [1]
 RP TISSUE=Needle;
 RC Plomion C., Costa P., Bahman N., Frigerio J.M.;
 RA Plomion C., Costa P., Bahman N., Frigerio J.M.;
 RT "Genetic analysis of needle proteins in maritime pine, 1. Mapping
 RT dominant and codominant protein markers assayed on diploid tissue, in
 RT a haploid-based genetic map.";
 RL Silvae Genetica 46:161-165(1997).
 RN [2]
 RP TISSUE=Needle;
 RC MEDLINE=99274088; PubMed=10344291;
 RX Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.5, ITS MW IS: 62 KDa.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;
 Query Match 18.4%; Score 21; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 26+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 SYNDE 12
 Db 9 SATNDE 14

RESULT 14
 CXAB_CONAL STANDARD; PRT; 16 AA.
 AC P56641;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Auitc.
 OS Conus aulicus (Court cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=89437;
 RN [1]
 RP TISSUE=Venom;
 RC MEDLINE=99003392; PubMed=9786965;
 RX Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
 RA Olivera B.M., McIntosh J.M.;
 RT "Alpha-conotoxin Auitc selectively blocks alpha3 beta4 nicotinic
 RT acetylcholine receptors and nicotine-evoked norepinephrine release.";
 RL J. Neurosci. 18:8571-8579(1998).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1667.6; METHOD=Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR HSSP: P50984; IPEN.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT DISULFID 3 3
 FT DISULFID 16 16
 MOD_RES 4 16
 AMIDATION.

SQ SEQUENCE 16 AA; 1673 MW; 1E310D3B8FDC7001 CRC64;
 Query Match 18.4%; Score 21; DB 1; Length 16;
 Best Local Similarity 28.6%; Pred. No. 2.1e+03;
 Matches 4; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 CCYDGSVNNDETC 14
 Db 3 CSYPCFATNSGYC 16

RESULT 15
 CXAB_CONPE STANDARD; PRT; 16 AA.
 AC P50985;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Pn1b.
 OS Conus pennaceus (Feathered cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=37335;
 RN [1]
 RP TISSUE=Venom;
 RC MEDLINE=94347719; PubMed=8068627;
 RX Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
 RA Spira M.E., Zlotkin E.;
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
 RT acetylcholine receptors.";
 RL Biochemistry 33:9523-9529(1994).
 RN [2]
 RP SULFATION OF TYR-15.
 RX MEDLINE=99242956; PubMed=10226369;
 RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
 RA Baldwin M.A., Burlingame A.L.;
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
 RT alpha-Pn1a and alpha-Pn1b: further investigation of labile sulfo- and
 RT phosphopeptides by electrospray, matrix-assisted laser
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
 RT spectrometry.";
 RL J. Mass Spectrom. 34:447-454(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RX MEDLINE=97443322; PubMed=9298951;
 RA Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
 RT "Crystal structure at 1.1-A resolution of alpha-conotoxin Pn1b:
 RT comparison with alpha-conotoxins Pn1a and Gt1.";
 RL Biochemistry 36:11323-11330(1997).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
 CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
 CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PDB: 1AKG; 20-MAY-98.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 3
 FT DISULFID 15 15
 FT DISULFID 16 16
 MOD_RES 16 16
 AMIDATION.
 SQ SEQUENCE 16 AA; 1643 MW; 05310F95ED86AF5 CRC64;
 Query Match 18.4%; Score 21; DB 1; Length 16;
 Best Local Similarity 21.4%; Pred. No. 2.1e+03;
 Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CCYDGSVNNDETC 14

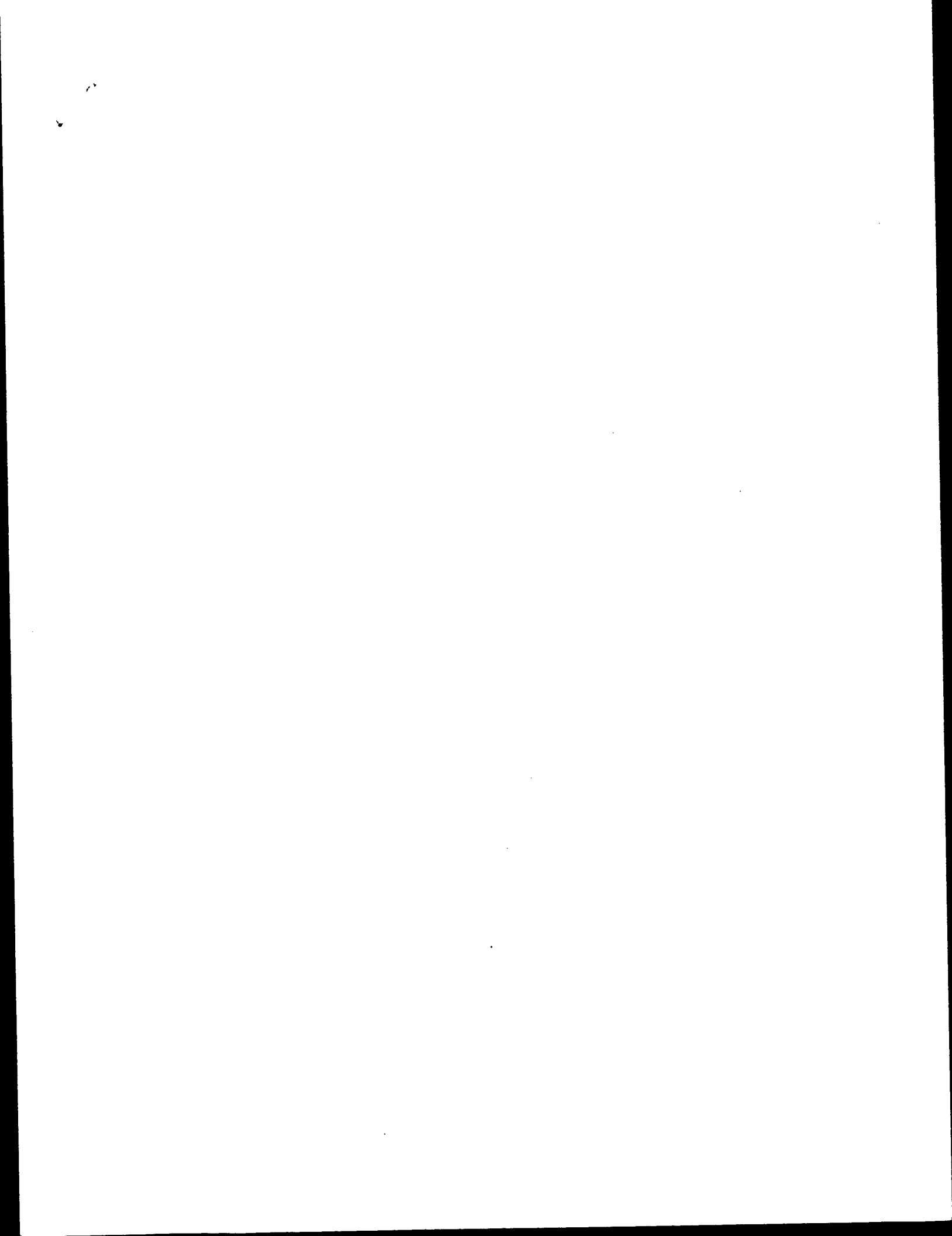
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Page 7

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Db 3 CSUPPCALSNPDYC 16

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Job time : 27 secs



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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:23:02 ; Search time 28 Seconds
(without alignments)
147.177 Million cell updates/sec

Title: US-09-651-685A-5

Perfect score: 114

Sequence: 1 CCYDGSVNNDETCEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 6395

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRAL:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	24.6	19	11	Q9QVJ9
2	26	22.8	16	6	Q8SPT4
3	26	22.8	17	15	Q78381
4	26	22.8	18	6	O46665
5	26	22.8	19	4	Q9UCD0
6	26	22.8	19	11	Q9QW83
7	25	21.9	15	4	Q9UCD0
8	24	21.1	18	6	Q9T781
9	24	21.1	20	5	P82201
10	24	21.1	18	2	O30888
11	23	20.2	18	2	O9R4F3
12	23	20.2	18	6	O97668
13	23	20.2	19	2	O9R511
14	23	20.2	20	4	O9UDF5
15	23	20.2	16	2	O47605
16	22.5	19.7	16	2	O47605

17	22	19.3	10	2	P96421	P96421 neisseria g
18	22	19.3	12	12	O85666	O85666 reovirus (t
19	22	19.3	15	11	Q9QVJ7	Q9QVJ7 rattus sp.
20	22	19.3	15	11	Q9QVJ8	Q9QVJ8 rattus sp.
21	22	19.3	18	4	Q9UM83	Q9UM83 homo sapien
22	22	19.3	18	6	Q95MX1	Q95MX1 syncerus ca
23	22	19.3	18	6	Q95MX0	Q95MX0 tragelaphus
24	22	19.3	18	6	Q95MW9	Q95MW9 oryx gazell
25	22	19.3	18	6	Q95MW8	Q95MW8 oryx dammah
26	22	19.3	18	6	Q95MW7	Q95MW7 hippotragus
27	22	19.3	18	6	Q95MW6	Q95MW6 bestragus h
28	22	19.3	18	6	Q95MW5	Q95MW5 alcelaphus
29	22	19.3	18	6	Q95MW4	Q95MW4 connochaete
30	22	19.3	18	6	Q95MW3	Q95MW3 redunda ful
31	22	19.3	18	6	Q95MW2	Q95MW2 redunda red
32	22	19.3	18	6	Q95MW1	Q95MW1 kobus leche
33	22	19.3	18	6	Q95MW0	Q95MW0 pelae capre
34	22	19.3	18	6	Q95MW9	Q95MW9 antidorcas
35	22	19.3	18	6	Q95MW8	Q95MW8 litocranius
36	22	19.3	18	6	Q95MW7	Q95MW7 raphicerus
37	22	19.3	18	6	Q95MW6	Q95MW6 raphicerus
38	22	19.3	18	6	Q95MW5	Q95MW5 neotragus m
39	22	19.3	18	6	Q95MW4	Q95MW4 neotragus m
40	22	19.3	18	6	Q95MW3	Q95MW3 cephalophus
41	22	19.3	18	6	Q95MW2	Q95MW2 sylvicapra
42	22	19.3	18	6	Q95MW1	Q95MW1 outrebia our
43	22	19.3	18	6	Q95MW0	Q95MW0 ratius norv
44	22	19.3	18	11	O63136	O63136 ratius norv
45	22	19.3	19	2	O35502	O35502 lactobacill

ALIGNMENTS

RESULT 1

ID	Q9QVJ9	PRELIMINARY:	PRT:	19 AA.
AC	Q9QVJ9	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Meprin-B peptide BI (Fragment).			
OS	Mus sp.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10095;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE-91373354; PubMed-1894622;			
RA	Kounnas M.Z., Wolz R.L., Gorbica C.M., Bond J.S.;			
RT	"Meprin-A and -B, Cell surface endopeptidases of the mouse kidney.";			
RL	J. Biol. Chem. 266:17350-17357(1991).			
FT	NON_TER 1			
FT	NON_TER 19			
FT	NON_TER 19			
SO	SEQUENCE 19 AA; 2157 MW; 81E66F19417E20C5 CRC64;			

Query Match Best Local Similarity 24.6%; Score 28; DB 11; Length 19;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 YDGSVNNDET 13
Db 1 ENQVSIINDT 11

RESULT 2

Q8SPT4
ID Q8SPT4
AC Q8SPT4
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chloride channel 2 (Fragment).

```

GN CLC2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
RN NCBI_TaxID=9544;
RP SEQUENCE FROM N.A.
RA Norrgren R.B. Jr., Zink M.A., Jia Y., Ojeda S.R., Spindel E.R.;
RT "Construction of a targeted Rhesus macaque microarray."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF489851; AAL96695.1;
FT NON_TER 1
SQ SEQUENCE 16 AA; 1691 MW; 50D83BF4FC6AF49E CRC64;

Query Match
Best Local Similarity 22.8%; Score 26; DB 6; Length 16;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGASVNDDECE 15
DB 5 EGSPSDSDCKQ 16

RESULT 3
078381
AC 078381; PRELIMINARY; PRT; 17 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Viral sample FLPBR5F (Florida patient B), partial env cds, V5 region
(Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN NCBI_TaxID=11676;
RP SEQUENCE FROM N.A.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=92271245; PubMed=1589796.
RA Ou C.-Y., Ciesielski C.A., Myers G., Banda C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
RA Economou A.N., Witte J.J., Furrman L.J., Salten G.A., Curran J.W.,
RA Jaffe H.W.;
RT "Molecular Epidemiology of HIV Transmission in a Dental Practice."
RL Science 256:1165-1171(1992).
DR EMBL: M82126; AAA44496.1;
FT NON_TER 1
SQ SEQUENCE 17 AA; 1708 MW; 347570D2D12CA370 CRC64;

Query Match
Best Local Similarity 22.8%; Score 26; DB 15; Length 17;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 GASVNDDET 13
DB 2 GNNTNMTET 10

RESULT 4
046665
AC 046665; PRELIMINARY; PRT; 18 AA.
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Glucose-6-phosphate dehydrogenase (Fragment).
OS Macropus robustus robustus.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
RN NCBI_TaxID=35580;
RP SEQUENCE FROM N.A.
RA MEDLINE=97224585; PubMed=9060417;
RT Analysis of the intron-exon structure of the G6PD gene of the
RT wallaroo (Macropus robustus) by polymerase chain reaction.
RL Mamm. Genome 8:146-147(1997).
DR EMBL: U53775; AAC48790.1;
DR InterPro: IPR001282; G6PD.
DR Pfam: PF02781; G6PD_C_1.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1992 MW; C6D5981B528258FB CRC64;

Query Match
Best Local Similarity 22.8%; Score 26; DB 6; Length 18;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 6 ASVNDDECEOR 17
DB 7 ASTNSDDVDRDEK 18

RESULT 5
090CD0
AC 090CD0; PRELIMINARY; PRT; 19 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE C215 antigen (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE.
RA Bjork P., Jonsson U., Svedberg H., Larsson K., Lind P., Dillner J.,
RA Hedlund G., Dohlsten M., Kalland T.;
RT "Isolation, partial characterization, and molecular cloning of a human
RT colon adenocarcinoma cell-surface glycoprotein recognized by the C215
RT mouse monoclonal antibody."
RL J. Biol. Chem. 268:24232-24241(1993).
SQ SEQUENCE 19 AA; 2042 MW; 54135D12119705E6 CRC64;

Query Match
Best Local Similarity 22.8%; Score 26; DB 4; Length 19;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DGASVND 11
DB 4 EGALQND 11

RESULT 6
090W83
AC 090W83; PRELIMINARY; PRT; 19 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE PHOSPHOPHORIN=PEPTIDE fragment 12-44 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RL MEDLINE=91291127; PubMed=2064607;

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RA Sabaay B., Stetler-Stevenson W.G., Lechner J.H., Veis A.;
 RT "Domain structure and sequence distribution in dentin phosphoporyn."
 RL Biochem. J. 276:659-707(1991).
 DR HSSP; P00760; 1A07.
 FT NON_TER 1
 SO SEQUENCE 19 AA; 2195 MW; 744603FE729FDE0C CRC64;

Query Match 22.8%; Score 26; DB 11; Length 19;
 Best Local Similarity 44.4%; Pred. No. 1.6e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YDGASVND 11
 DB 7 YNSNTLND 15

RESULT 7

09UCC0 PRELIMINARY; PRT; 15 AA.
 AC 09UCC0;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE Insulin-like growth factor receptor alpha subunit (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94079885; PubMed=8257688;
 RA Kasuya J., Paz I.B., Maddux B.A., Goldfine I.D., Hefta S.A.,
 RA Fujita-Yamaguchi Y.;
 RT "Characterization of human placental insulin-like growth factor-
 RT I/insulin hybrid receptors by proteoln microsequencing and
 RT purification."
 RL Biochemistry 32:13531-13536(1993).
 SO SEQUENCE 15 AA; 1721 MW; 98BC151D6D81784B CRC64;

Query Match 21.9%; Score 25; DB 4; Length 15;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 CYDGASVND 11
 DB 3 CGPGIDIRND 12

RESULT 8

09TT81 PRELIMINARY; PRT; 18 AA.
 AC 09TT81;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Wilm's tumor protein 1 (Fragment).
 GN WT1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21015404; PubMed=11130975;
 RA Brouillette J.A., Andrew J.R., Venna P.J.;
 RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
 RT method."
 RL Mamm. Genome 11:1079-1086(2000).
 DR EMBL; AF201736; AAF19824.1; -.
 FT NON_TER 1
 SO SEQUENCE 18 AA; 2215 MW; A3C1EPD3F1350767 CRC64;

SO SEQUENCE 18 AA; 2196 MW; 1EE8DAD8E072C0BF CRC64;

Query Match 21.1%; Score 24; DB 6; Length 18;
 Best Local Similarity 33.3%; Pred. No. 3.3e+03;
 Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 12 ETCEGRAR 20
 DB 7 KTCQKFRS 15

RESULT 9

016188 PRELIMINARY; PRT; 20 AA.
 AC 016188;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Adenosine deaminase protein (Fragment).
 GN ADENOSINE DEAMINASE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94327968; PubMed=8051429;
 RA Shovlin C.L., Simmonds H.A., Fairbanks L.D., Deacock S.J.,
 RA Hughes J.M., Lechner R.I., Webster A.D., Sun X.M., Webb J.C.,
 RA Soutar A.K.;
 RT "Adult onset immunodeficiency caused by inherited adenosine deaminase
 RT deficiency."
 RL J. Immunol. 153:2331-2339(1994).
 DR EMBL; S72469; AAD14102.1; -.
 FT NON_TER 1
 SO SEQUENCE 20 AA; 2175 MW; 4EABA6143F73984C CRC64;

Query Match 21.1%; Score 24; DB 4; Length 20;
 Best Local Similarity 50.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 13 TCCEGRAR 20
 DB 12 SCEVRCRS 19

RESULT 10

P82201 PRELIMINARY; PRT; 20 AA.
 AC P82201;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Dityria;
 OC Bombycoidea; Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE.
 RX STRAIN=XINHANG X KEMING; TISSUE=BODY WALL, AND FAT BODY;
 RX MEDLINE=21177481; PubMed=11280994;
 RA Zhong B.X.;
 RT "Protein database for several tissues derived from five instar of
 RT silkworm."
 RL I Chuan Hsueh Pao 28:217-224(2001).
 CC -I- SIMILARITY: TO THE N-TERMINAL OF TROPOMYOSINS.
 FT NON_TER 20
 SO SEQUENCE 20 AA; 2215 MW; A3C1EPD3F1350767 CRC64;

Query Match 21.1%; Score 24; DB 5; Length 20;
 Best Local Similarity 80.0%; Pred. No. 3.7e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 CEORA 18
111:1
Db 5 CEQQA 9

RESULT 11

ID 030888 PRELIMINARY; PRT; 18 AA.
AC 030888;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Nodulation protein (Fragment).
GN NODA.
OS Bradyrhizobium sp.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_Taxid=376;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20020861; PubMed=10553291;
RA Steiner J.P., Parker M.A.;
RT "Diversity and relationships of Bradyrhizobia from Amphicarpa
RT bracteata based on partial nod and ribosomal sequences.";
RL Syst. Appl. Microbiol. 22:387-392(1999).
DR EMBL; AF020680; AAB71696.1; -.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1943 MW; C8C595DCD14D7A5F CRC64;

Query Match 20.2%; Score 23; DB 2; Length 18;
Best Local Similarity 28.6%; Pred. No. 4.8e+03;
Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 SVNNDETCQRAAR 20
:: 1:11
Db 2 NIPGSRSAESRSAR 15

RESULT 12

ID 09R4F3 PRELIMINARY; PRT; 18 AA.
AC 09R4F3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE 20 kDa fimbrial adhesin subunit (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE.
RX MEDLINE=96110952; PubMed=8557360;
RA Berlin Y., Girardeau J.P., Darfeuille-Michaud A., Contepois M.;
RT "Characterization of 20k fimbria, a new adhesin of septicemic and
RT diarrhoea-associated Escherichia coli strains, that belongs to a family
RT of adhesins with N-acetyl-D-glucosamine recognition.";
RL Infect. Immun. 64:332-342(1996).
SQ SEQUENCE 18 AA; 1990 MW; 79AF96A13476DF81 CRC64;

Query Match 20.2%; Score 23; DB 2; Length 18;
Best Local Similarity 35.7%; Pred. No. 4.8e+03;
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 YDASVNNDETCQ 16
111 1:1
Db 1 YDGTINNGKVVQD 14

RESULT 13
097668

ID 097668 PRELIMINARY; PRT; 18 AA.

AC 097668;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Brandon R.B., Giffard J.M., Bell T.K.;
RT "Isolation of Equine Lactoferrin Gene.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF102025; AAC77463.1; -.
DR HSSP; 077698; ICE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1936 MW; D8FBFA226AA6DD9 CRC64;

Query Match 20.2%; Score 23; DB 6; Length 18;
Best Local Similarity 66.7%; Pred. No. 4.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGA 6
111 1
Db 1 CLQDGA 6

RESULT 14

ID 09R511 PRELIMINARY; PRT; 19 AA.
AC 09R511;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Nitrite hydratase alpha subunit (Fragment).
OS Brevibacterium.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Micrococciaceae; Brevibacteriaceae.
OX NCBI_Taxid=1696;
RN [1]
RP SEQUENCE.
RX MEDLINE=92407758; PubMed=1527703;
RA Duran R., Chion C.K., Bigey F., Arnaud A., Galzy P.;
RT "The N-terminal amino acid sequences of Brevibacterium sp. R312
RT nitrite hydratase.";
RL J. Basic Microbiol. 32:13-19(1992).
SQ SEQUENCE 19 AA; 1923 MW; 84726D1A1282FB63 CRC64;

Query Match 20.2%; Score 23; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 5.1e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 7 SVNNDETCQRA 18
111 1:1
Db 1 SVTIDHTTENNA 12

RESULT 15

ID 09UDF5 PRELIMINARY; PRT; 20 AA.
AC 09UDF5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DIPEPTIDYLPEPTIDASE IV (EC 3.4.14.5) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID-9606;
RN (1)
RP SEQUENCE
RX MEDLINE-95294018; PubMed-7539799;
RA Duke-Cohan J.S., Morimoto C., Rocker J.A., Schlossman S.F.;
RT "A novel form of dipeptidylpeptidase IV found in human serum.
RT Isolation, characterization, and comparison with T lymphocyte membrane
RT dipeptidylpeptidase IV (CD26).";
RL J. Biol. Chem. 270:14107-14114(1995).
SQ SEQUENCE 20 AA; 2274 MW; 764B669537DB8AB0 CRC64;

Query Match 20.2%; Score 23; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 5.4e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVND 11
|| : ||
Db 7 CYCTANTND 16

Search completed: May 1, 2003, 22:27:18
Job time : 29 secs

GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:20:12 ; Search time 74 Seconds

(without alignments)
36.014 Million cell updates/sec

Title: US-09-651-685a-5
Perfect score: 114
Sequence: 1 CCGAGASVNDPCEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 289567

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_101002.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	22 AAB74055	Human C5a peptide
2	111	97.4	20	22 AAB74111	C-terminal truncat
3	110	96.5	20	22 AAB74110	C-terminal truncat
4	110	96.5	20	22 AAB74112	C-terminal truncat
5	110	96.5	20	22 AAB74113	C-terminal truncat
6	110	96.5	20	22 AAB74114	C-terminal truncat
7	110	96.5	20	22 AAB74115	C-terminal truncat
8	110	96.5	20	22 AAB74116	C-terminal truncat
9	109	95.6	20	22 AAB74097	C-terminal truncat
10	108	94.7	20	22 AAB74107	C-terminal truncat

11	108	94.7	20	22 AAB74108	C-terminal truncat
12	106	93.0	20	22 AAB74115	C-terminal truncat
13	105	92.1	18	22 AAB74098	C-terminal truncat
14	105	92.1	19	22 AAB74102	C-terminal truncat
15	102	89.5	20	22 AAB74109	C-terminal truncat
16	101	88.6	17	22 AAB74099	C-terminal truncat
17	98	86.0	20	22 AAB74117	C-terminal truncat
18	96	84.2	16	22 AAB74100	C-terminal truncat
19	96	84.2	18	22 AAB74103	C-terminal truncat
20	91	79.8	15	22 AAB74101	C-terminal truncat
21	89	78.1	17	22 AAB74104	C-terminal truncat
22	83	72.8	15	22 AAB74105	C-terminal truncat
23	77	67.5	15	22 AAB74106	C-terminal truncat
24	51	44.7	20	22 AAB74052	C-terminal truncat
25	40.5	35.5	18	21 AAB21536	C-terminal truncat
26	38.5	33.8	16	21 AAB21533	C-terminal truncat
27	38.5	33.8	20	21 AAB21498	C-terminal truncat
28	38	33.3	16	21 AAB75274	C-terminal truncat
29	38	33.3	16	21 AAB21522	C-terminal truncat
30	36	31.6	15	21 AAB80449	C-terminal truncat
31	35.5	31.1	17	21 AAB21549	C-terminal truncat
32	35	30.7	16	18 AAM24881	C-terminal truncat
33	35	30.7	16	18 AAM24881	C-terminal truncat
34	34.5	30.3	18	16 AAR75292	C-terminal truncat
35	34.5	30.3	18	16 AAM24897	C-terminal truncat
36	34.5	30.3	18	18 AAM12751	C-terminal truncat
37	34	29.8	15	18 AAR30137	C-terminal truncat
38	34	29.8	19	15 AAR56639	C-terminal truncat
39	34	29.8	19	15 AAR56633	C-terminal truncat
40	34	29.8	19	16 AAR75281	C-terminal truncat
41	34	29.8	19	18 AAM30153	C-terminal truncat
42	34	29.8	19	18 AAM30136	C-terminal truncat
43	34	29.8	19	18 AAM21743	C-terminal truncat
44	33.5	29.4	18	21 AAB21411	C-terminal truncat
45	33	28.9	21	21 AAB21512	C-terminal truncat

ALIGNMENTS

RESULT 1
ID AAB74055 standard; Peptide: 20 AA.
AC AAB74055;
DT 16-MAY-2001 (first entry)
XX
DE Human C5a peptide fragment #2.
XX
KW Human; C5a; complement; antibody; bacterial infection; sinusitis;
KW meningitis; respiratory; gastrointestinal; urinary tract infection;
KW wound; anaphylatoxin; sepsis.
XX
OS Homo sapiens.
XX
PN W0200115731-A1.
XX
PD 08-MAR-2001.
XX
PF 31-AUG-2000; 2000MO-US24219.
XX
PR 31-AUG-1999; 99US-0387671.
XX
(UNMI) UNIV MICHIGAN.
XX
PI Ward PA, Huber-Lang M, Sarma V;
XX WPI: 2001-226665/23.
XX N-PSDB: AAF75793.
XX
PT Compositions for treating blood-borne and toxin mediated diseases and treatment of sepsis in humans and other animals comprises anti-C5a

PT antibodies generated against C-terminal truncated C5a peptides -
 XX
 PS Claim 8; Page 26; 84pp; English.

CC The present sequence is a peptide fragment of human complement component
 CC C5a (the full-length sequence is given in AAB74053). The present
 CC invention relates to an antibody specific for the present sequence. The
 CC C5a-antibody can be used in a therapeutic composition, which is useful
 CC for treating a subject suffering from bacterial infection, e.g.
 CC sinusitis, meningitis, respiratory, gastrointestinal or urinary tract
 CC infections or infections in wounds. In addition, the C5a antibody can
 CC be used for treating sepsis. C5a is also known as anaphylatoxin.
 XX

SQ Sequence 20 AA;

Query Match 100.0%; Score 114; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.5e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
 |||||
 DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 2

AAB74111
 ID AAB74111 standard; Peptide; 20 AA.

XX AAB74111;

XX 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #49.

XX C5a; complement; antibody; bacterial infection; sinusitis;

KW meningitis; respiratory; gastrointestinal; urinary tract infection;

KW wound; anaphylatoxin; sepsis.

XX Unidentified.

XX WO200115731-A1.

XX 08-MAR-2001.

PF 31-AUG-2000; 2000WO-US24219.

XX 31-AUG-1999; 99US-0387671.

XX (UNMI) UNIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX WPI; 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and
 PT treatment of sepsis in humans and other animals comprises anti-C5a
 PT antibodies generated against C-terminal truncated C5a peptides -

XX Disclosure; Page 30; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The
 CC present invention relates to an antibody specific for the present
 CC sequence. The C5a-antibody can be used in a therapeutic composition,
 CC which is useful for treating a subject suffering from bacterial
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
 CC urinary tract infections or infections in wounds. In addition, the C5a
 CC antibody can be used for treating sepsis. C5a is also known as
 CC anaphylatoxin.
 XX

SQ Sequence 20 AA;

Query Match 97.4%; Score 111; DB 22; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e-10;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
 |||||
 DB 1 CCYDGATVNNDETCEQRAAR 20

RESULT 3

AAB74110
 ID AAB74110 standard; Peptide; 20 AA.

XX AAB74110;

XX 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #48.

XX C5a; complement; antibody; bacterial infection; sinusitis;

KW meningitis; respiratory; gastrointestinal; urinary tract infection;

KW wound; anaphylatoxin; sepsis.

XX Unidentified.

XX WO200115731-A1.

XX 08-MAR-2001.

PF 31-AUG-2000; 2000WO-US24219.

XX 31-AUG-1999; 99US-0387671.

XX (UNMI) UNIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX WPI; 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and
 PT treatment of sepsis in humans and other animals comprises anti-C5a
 PT antibodies generated against C-terminal truncated C5a peptides -

XX Disclosure; Page 30; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The
 CC present invention relates to an antibody specific for the present
 CC sequence. The C5a-antibody can be used in a therapeutic composition,
 CC which is useful for treating a subject suffering from bacterial
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
 CC urinary tract infections or infections in wounds. In addition, the C5a
 CC antibody can be used for treating sepsis. C5a is also known as
 CC anaphylatoxin.
 XX

SQ Sequence 20 AA;

Query Match 96.5%; Score 110; DB 22; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.9e-10;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
 |||||
 DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 4

AAB74112
 ID AAB74112 standard; Peptide; 20 AA.

XX AAB74112;

XX 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #50.

KW	C5a; complement; antibody; bacterial infection; sinusitis;
KM	meningitis; respiratory; gastrointestinal; urinary tract infection;
KM	wound; anaphylatoxin; sepsis.
OS	Unidentified.
PN	WO200115731-A1.
XX	
PD	08-MAR-2001.
PF	31-AUG-2000; 2000MO-US24219.
XX	
PR	31-AUG-1999; 99US-0387671.
XX	
PA	(UNMI) UNIV MICHIGAN.
PI	Ward PA, Huber-Lang M, Sarma V;
XX	
DR	WPI: 2001-226665/23.
PT	Compositions for treating blood-borne and toxin mediated diseases and
PT	treatment of sepsis in humans and other animals comprises anti-C5a
PT	antibodies generated against C-terminal truncated C5a peptides -
PS	Disclosure: Page 30; 84pp; English.
CC	The present sequence is a C-terminal truncated C5a peptide fragment. The
CC	present invention relates to an antibody specific for the present
CC	sequence. The C5a-antibody can be used in a therapeutic composition,
CC	which is useful for treating a subject suffering from bacterial
CC	infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC	urinary tract infections or infections in wounds. In addition, the C5a
CC	antibody can be used for treating sepsis. C5a is also known as
CC	anaphylatoxin.
SQ	Sequence 20 AA:
QY	Query Match Best Local Similarity 96.5%; Score 110; DB 22; Length 20; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB	1 CCYDGSVNNDETCEQRRAAR 20 1 CCYDGSVNNDETCEQRRAAR 20
RESULT 5	
AAB74113	
ID	AAB74113 standard; Peptide: 20 AA.
XX	
AC	AAB74113:
XX	
DT	16-MAY-2001 (first entry)
DE	C-terminal truncated C5a peptide #51.
XX	
KM	C5a; complement; antibody; bacterial infection; sinusitis;
KM	meningitis; respiratory; gastrointestinal; urinary tract infection;
KM	wound; anaphylatoxin; sepsis.
OS	Unidentified.
PN	WO200115731-A1.
XX	
PD	08-MAR-2001.
XX	
PF	31-AUG-2000; 2000MO-US24219.
XX	
PR	31-AUG-1999; 99US-0387671.
XX	
PA	(UNMI) UNIV MICHIGAN.
PI	Ward PA, Huber-Lang M, Sarma V;
XX	

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XX
DR WPI: 2001-226665/23.
XX
PT Compositions for treating blood-borne and toxin mediated diseases and
PT treatment of sepsis in humans and other animals comprises anti-C5a
PT antibodies generated against C-terminal truncated C5a peptides -
XX
PS Disclosure; Page 30; 84pp; English.
XX
CC The present sequence is a C-terminal truncated C5a peptide fragment. The
CC present invention relates to an antibody specific for the present
CC sequence. The C5a-antibody can be used in a therapeutic composition,
CC which is useful for treating a subject suffering from bacterial
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC urinary tract infections or infections in wounds. In addition, the C5a
CC antibody can be used for treating sepsis. C5a is also known as
CC anaphylatoxin.
XX
SQ Sequence 20 AA:
XX
Query Match 96.5%; Score 110; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. NO. 1.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCYDGASVNNDETCEORAR 20
| | | | | | | | | | | | | | | | | |
DB 1 CCYDGASANNDETCEORAR 20
RESULT 6
AAB74114
ID AAB74114 standard; Peptide: 20 AA.
XX
AC AAB74114;
XX
DT 16-MAY-2001 (first entry)
XX
DE C-terminal truncated C5a peptide #52.
XX
KW C5a; Complement; antibody; bacterial infection; sinusitis;
KW meningitis; respiratory; gastrointestinal; urinary tract infection;
KW wound; anaphylatoxin; sepsis.
XX
OS Unidentified.
XX
XX
XX WO200115731-A1.
XX
XX 08-MAR-2001.
XX
XX 31-AUG-2000; 2000WO-US24219.
XX
XX 31-AUG-1999; 9905-0387671.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX
XX Ward PA, Huber-Ilang M, Sarma V;
XX
XX WPI: 2001-226665/23.
XX
XX Compositions for treating blood-borne and toxin mediated diseases and
XX treatment of sepsis in humans and other animals comprises anti-C5a
XX antibodies generated against C-terminal truncated C5a peptides -
XX
XX Disclosure; Page 30; 84pp; English.
XX
XX The present sequence is a C-terminal truncated C5a peptide fragment. The
XX present invention relates to an antibody specific for the present
XX sequence. The C5a-antibody can be used in a therapeutic composition,
XX which is useful for treating a subject suffering from bacterial
XX infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
XX urinary tract infections or infections in wounds. In addition, the C5a
XX antibody can be used for treating sepsis. C5a is also known as
XX anaphylatoxin.

```

XX
SQ Sequence 20 AA:

Query Match 96.5%; Score 110; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAR 20
DB 1 CCYDGASVNNDETCEQRAR 20

RESULT 7
AAB74116

ID AAB74116 standard; Peptide: 20 AA.

AC AAB74116;

DT 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #54.

XX C5a; complement; antibody; bacterial infection; sinusitis;
KW meningitis; respiratory; gastrointestinal; urinary tract infection;
KM wound; anaphylatoxin; sepsis.

XX Unidentified.

OS WO200115731-A1.

XX 08-MAR-2001.

XX 31-AUG-2000; 2000WO-US24219.

XX 31-AUG-1999; 99US-0387671.

XX (UNMI) UNIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX WPI: 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and
PT treatment of sepsis in humans and other animals comprises anti-C5a
PT antibodies generated against C-terminal truncated C5a peptides

XX Disclosure; Page 30; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The
CC present invention relates to an antibody specific for the present
CC sequence. The C5a-antibody can be used in a therapeutic composition,
CC which is useful for treating a subject suffering from bacterial
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC urinary tract infections or infections in wounds. In addition, the C5a
CC antibody can be used for treating sepsis. C5a is also known as
CC anaphylatoxin.

XX Sequence 20 AA:

Query Match 96.5%; Score 110; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAR 20
DB 1 CCYDGASVNNDETCEQRAR 20

RESULT 8
AAB74097

ID AAB74097 standard; Peptide: 19 AA.

XX AAB74097;

XX 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #35.

XX C5a; complement; antibody; bacterial infection; sinusitis;
KW meningitis; respiratory; gastrointestinal; urinary tract infection;
KM wound; anaphylatoxin; sepsis.

XX Unidentified.

OS WO200115731-A1.

XX 08-MAR-2001.

XX 31-AUG-2000; 2000WO-US24219.

XX 31-AUG-1999; 99US-0387671.

XX (UNMI) UNIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX WPI: 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and
PT treatment of sepsis in humans and other animals comprises anti-C5a
PT antibodies generated against C-terminal truncated C5a peptides
PS Disclosure; Page 30; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The
CC present invention relates to an antibody specific for the present
CC sequence. The C5a-antibody can be used in a therapeutic composition,
CC which is useful for treating a subject suffering from bacterial
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC urinary tract infections or infections in wounds. In addition, the C5a
CC antibody can be used for treating sepsis. C5a is also known as
CC anaphylatoxin.

XX Sequence 19 AA:

Query Match 95.6%; Score 109; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRA 19
DB 1 CCYDGASVNNDETCEQRA 19

RESULT 9
AAB74120

ID AAB74120 standard; Peptide: 20 AA.

XX AAB74120;

XX 16-MAY-2001 (first entry)

XX Human C5a peptide fragment #7.

XX Human; C5a; complement; antibody; bacterial infection; sinusitis;
KW meningitis; respiratory; gastrointestinal; urinary tract infection;
KM wound; anaphylatoxin; sepsis.

XX Homo sapiens.

OS WO200115731-A1.

XX 08-MAR-2001.

XX 31-AUG-2000; 2000WO-US24219.

RESULT 12
 AAB74115 standard; Peptide: 20 AA.
 ID AAB74115;
 AC AAB74115;
 XX
 DT 16-MAY-2001 (first entry)
 DE C-terminal truncated C5a peptide #53.
 XX
 DE C-terminal truncated C5a peptide #53.
 XX
 KW C5a; complement; antibody; bacterial infection; sinusitis;
 KM meningitis; respiratory; gastrointestinal; urinary tract infection;
 KM wound; anaphylatoxin; sepsis.
 XX
 OS Unidentified.
 XX
 PN WO200115731-A1.
 XX
 PD 08-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-US24219.
 XX
 PR 31-AUG-1999; 99US-0387671.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Ward PA, Huber-Lang M, Sarma V;
 XX
 DR WPI; 2001-226665/23.
 XX
 PT Compositions for treating blood-borne and toxin mediated diseases and
 PT treatment of sepsis in humans and other animals comprises anti-C5a
 PT antibodies generated against C-terminal truncated C5a peptides -
 XX
 PS Disclosure; Page 30; 84pp; English.
 XX
 CC The present sequence is a C-terminal truncated C5a peptide fragment. The
 CC present invention relates to an antibody specific for the present
 CC sequence. The C5a-antibody can be used in a therapeutic composition,
 CC which is useful for treating a subject suffering from bacterial
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
 CC urinary tract infections or infections in wounds. In addition, the C5a
 CC antibody can be used for treating sepsis. C5a is also known as
 CC anaphylatoxin.
 CC
 XX
 SQ Sequence 20 AA;
 Query Match 93.0%; Score 106; DB 22; Length 20;
 Best Local Similarity 90.0%; Pred. No. 8, 1e-10;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCYDGASVNDTCCEQRAAR 20
 DB 1 CCYDGASVNDTCCEQRYVR 20
 RESULT 13
 AAB74098
 ID AAB74098 standard; Peptide: 18 AA.
 AC AAB74098;
 XX
 DT 16-MAY-2001 (first entry)
 DE C-terminal truncated C5a peptide #36.
 XX
 DE C-terminal truncated C5a peptide #36.
 XX
 KW C5a; complement; antibody; bacterial infection; sinusitis;
 KM meningitis; respiratory; gastrointestinal; urinary tract infection;
 KM wound; anaphylatoxin; sepsis.
 XX
 OS Unidentified.
 XX
 PN WO200115731-A1;
 XX

XX
 PD 08-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-US24219.
 XX
 PR 31-AUG-1999; 99US-0387671.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Ward PA, Huber-Lang M, Sarma V;
 XX
 DR WPI; 2001-226665/23.
 XX
 PT Compositions for treating blood-borne and toxin mediated diseases and
 PT treatment of sepsis in humans and other animals comprises anti-C5a
 PT antibodies generated against C-terminal truncated C5a peptides -
 XX
 PS Disclosure; Page 30; 84pp; English.
 XX
 CC The present sequence is a C-terminal truncated C5a peptide fragment. The
 CC present invention relates to an antibody specific for the present
 CC sequence. The C5a-antibody can be used in a therapeutic composition,
 CC which is useful for treating a subject suffering from bacterial
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
 CC urinary tract infections or infections in wounds. In addition, the C5a
 CC antibody can be used for treating sepsis. C5a is also known as
 CC anaphylatoxin.
 CC
 XX
 SQ Sequence 18 AA;
 Query Match 92.1%; Score 105; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCYDGASVNDTCCEQRA 18
 DB 1 CCYDGASVNDTCCEQRA 18
 RESULT 14
 AAB74102
 ID AAB74102 standard; Peptide: 19 AA.
 AC AAB74102;
 XX
 DT 16-MAY-2001 (first entry)
 DE C-terminal truncated C5a peptide #40.
 XX
 DE C-terminal truncated C5a peptide #40.
 XX
 KW C5a; complement; antibody; bacterial infection; sinusitis;
 KM meningitis; respiratory; gastrointestinal; urinary tract infection;
 KM wound; anaphylatoxin; sepsis.
 XX
 OS Unidentified.
 XX
 PN WO200115731-A1.
 XX
 PD 08-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-US24219.
 XX
 PR 31-AUG-1999; 99US-0387671.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Ward PA, Huber-Lang M, Sarma V;
 XX
 DR WPI; 2001-226665/23.
 XX
 PT Compositions for treating blood-borne and toxin mediated diseases and
 PT treatment of sepsis in humans and other animals comprises anti-C5a
 PT antibodies generated against C-terminal truncated C5a peptides -

PS Disclosure: Page 30; 84pp; English.

XX
CC The present sequence is a C-terminal truncated C5a peptide fragment. The
CC present invention relates to an antibody specific for the present
CC sequence. The C5a-antibody can be used in a therapeutic composition,
CC which is useful for treating a subject suffering from bacterial
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC urinary tract infections or infections in wounds. In addition, the C5a
CC antibody can be used for treating sepsis. C5a is also known as
XX anaphylatoxin.

SQ Sequence: 19 AA:

Query Match 92.1%; Score 105; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CYDGASVNNDETCEQRAAR 20
|||
Db 1 CYDGASVNNDETCEQRAAR 19

RESULT 15

AAB74109
ID AAB74109 standard; Peptide: 20 AA.

AC AAB74109;

DT 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #47.

KW C5a: complement; antibody; bacterial infection; sinusitis;
KM meningitis; respiratory; gastrointestinal; urinary tract infection;
KW wound; anaphylatoxin; sepsis.

OS Unidentified.

XX WO200115731-A1.

PD 08-MAR-2001.

PF 31-AUG-2000; 2000MO-US24219.

PR 31-AUG-1999; 99US-0387671.

PA (UNMI) UNIV MICHIGAN.

PI Ward PA, Huber-Lang M, Sarma V;

WPI: 2001-226665/23.

PT Compositions for treating blood-borne and toxin mediated diseases and
PT treatment of sepsis in humans and other animals comprises anti-C5a
PT antibodies generated against C-terminal truncated C5a peptides -

PS Disclosure: Page 30; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The
CC present invention relates to an antibody specific for the present
CC sequence. The C5a-antibody can be used in a therapeutic composition,
CC which is useful for treating a subject suffering from bacterial
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC urinary tract infections or infections in wounds. In addition, the C5a
CC antibody can be used for treating sepsis. C5a is also known as
XX anaphylatoxin.

SQ Sequence: 20 AA:

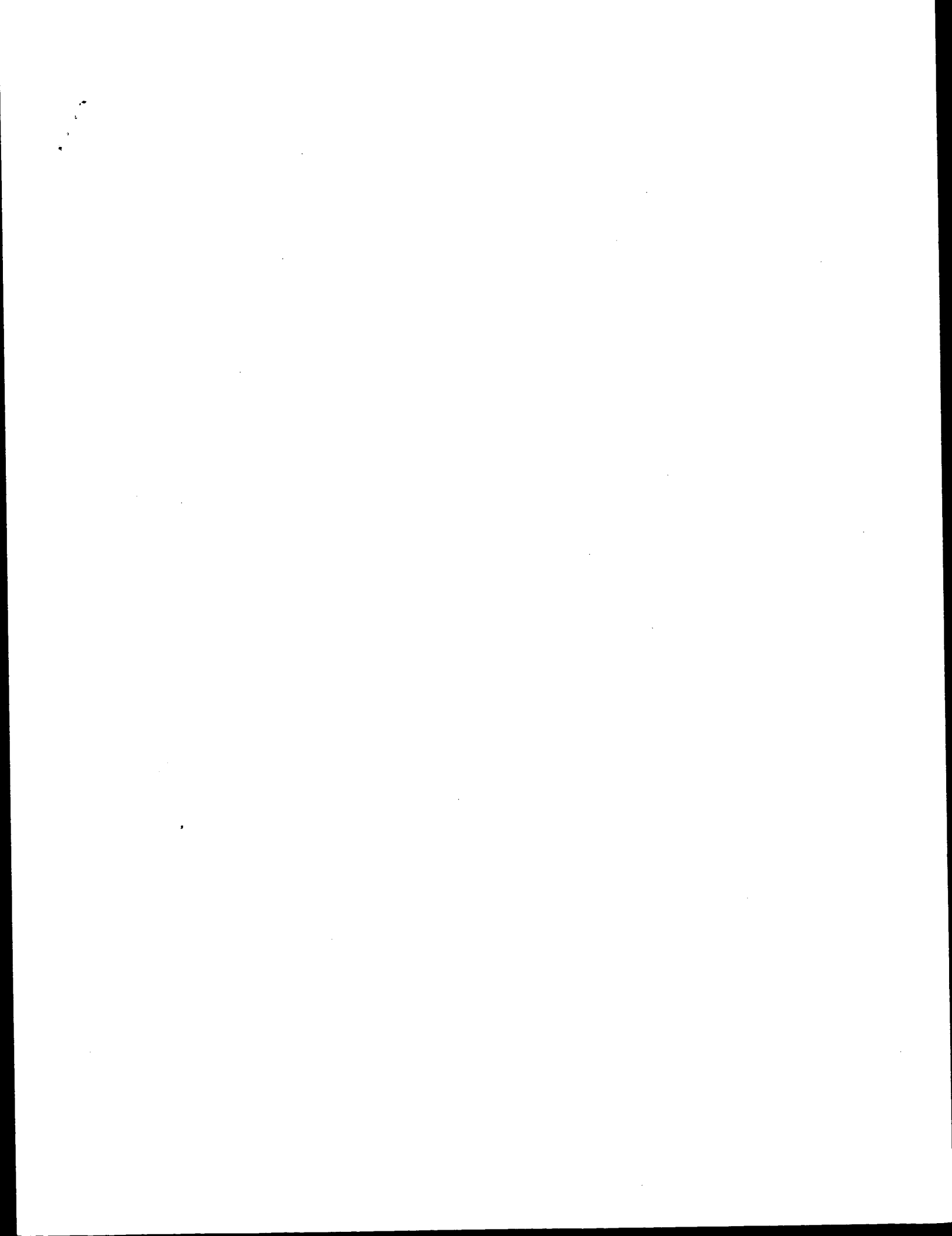
Query Match 89.5%; Score 102; DB 22; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.4e-09;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETCEQRAAR 20

Db 1 CCYDGASVNNDETCEQRAAR 20

Search completed: May 1, 2003, 22:26:11
Job time : 75 secs



GenCore version 5.1.4_p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 1, 2003, 22:27:23 ; Search time 45 Seconds
(without alignments)
38.350 Million cell updates/sec

Title: US-09-651-685a-5
Sequence: 1 CCYDASVNDCTCEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328255 segs, 86286685 residues
Total number of hits satisfying chosen parameters: 62178

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	111	97.4	20	9	US-09-878-603-68
3	110	96.5	20	9	US-09-878-603-67
4	110	96.5	20	9	US-09-878-603-69
5	110	96.5	20	9	US-09-878-603-70
6	110	96.5	20	9	US-09-878-603-71
7	110	96.5	20	9	US-09-878-603-73
8	109	95.6	20	9	US-09-878-603-54
9	108	94.7	20	9	US-09-878-603-64
10	108	94.7	20	9	US-09-878-603-65
11	106	93.0	20	9	US-09-878-603-72
12	105	92.1	18	9	US-09-878-603-55
13	105	92.1	19	9	US-09-878-603-59
14	102	89.5	20	9	US-09-878-603-66
15	101	88.6	17	9	US-09-878-603-56
16	98	86.0	20	9	US-09-878-603-74
17	96	84.2	16	9	US-09-878-603-57
18	96	84.2	18	9	US-09-878-603-60
19	91	79.8	15	9	US-09-878-603-58

20	89	78.1	17	9	US-09-878-603-61	Sequence 61, Appl
21	83	72.8	16	9	US-09-878-603-62	Sequence 62, Appl
22	77	67.5	15	9	US-09-878-603-63	Sequence 63, Appl
23	51	44.7	20	9	US-09-878-603-2	Sequence 2, Appl
24	34	29.8	20	10	US-09-321-801-5	Sequence 5, Appl
25	32	28.1	6	9	US-09-878-603-15	Sequence 15, Appl
26	30.5	26.8	16	9	US-10-084-994-16	Sequence 16, Appl
27	29	25.4	9	9	US-09-252-150-78	Sequence 78, Appl
28	29	25.4	10	10	US-09-779-308-42	Sequence 42, Appl
29	29	25.4	14	9	US-09-908-741-108	Sequence 108, Appl
30	28	24.6	6	9	US-09-878-603-25	Sequence 25, Appl
31	28	24.6	6	9	US-09-878-603-27	Sequence 27, Appl
32	28	24.6	7	10	US-09-873-676-84	Sequence 84, Appl
33	28	24.6	11	10	US-09-873-676-32	Sequence 32, Appl
34	28	24.6	18	10	US-09-734-520-23	Sequence 23, Appl
35	28	24.6	18	12	US-10-012-034A-23	Sequence 23, Appl
36	28	24.6	20	10	US-09-731-221-66	Sequence 66, Appl
37	27.5	24.1	20	9	US-09-910-009A-211	Sequence 211, Appl
38	27	23.7	17	10	US-09-864-761-47743	Sequence 4743, A
39	26.5	23.2	14	10	US-09-854-188-8	Sequence 8, Appl
40	26.5	23.2	16	9	US-09-910-009A-370	Sequence 370, Appl
41	26.5	23.2	18	9	US-09-908-741-22	Sequence 22, Appl
42	26	22.8	6	9	US-09-878-603-24	Sequence 24, Appl
43	26	22.8	7	9	US-09-917-788-4	Sequence 4, Appl
44	26	22.8	11	10	US-09-791-946-5	Sequence 5, Appl
45	26	22.8	12	9	US-10-156-932-79	Sequence 79, Appl

ALIGNMENTS

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RESULT 1
US-09-878-603-5
; Sequence 5, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czerniak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878, 603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387, 671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-878-603-5

Query Match      100.0%  Score 114;  DB 9;  Length 20;
Best Local Similarity 100.0%  Pred. No. 2.4e-10;
Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 CCYDASVNDCTCEQRAAR 20
DB      1 CCYDASVNDCTCEQRAAR 20

RESULT 2
US-09-878-603-68
; Sequence 68, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czerniak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis

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; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 68
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-68

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Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
Db 1 CCYDGATVNNDETCEQRAAR 20

RESULT 3
US-09-878-603-67
; Sequence 67, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 67
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-67

Query Match
Best Local Similarity 96.5%; Score 110; DB 9; Length 20;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
Db 1 CCYDGASVNNDETCEQRAAR 20

RESULT 4
US-09-878-603-69
; Sequence 69, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
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; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 69
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-69

Query Match
Best Local Similarity 96.5%; Score 110; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
Db 1 CCYDGASVNNDETCEQRAAR 20

RESULT 5
US-09-878-603-70
; Sequence 70, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 70
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-70

Query Match
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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
Db 1 CCYDGASVNNDETCEQRAAR 20

RESULT 6
US-09-878-603-71
; Sequence 71, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 71
; LENGTH: 20
; TYPE: PRT
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-71

Query Match
Best Local Similarity 96.5%; Score 110; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 1 CCYDGASVNNDETCEORAR 20

RESULT 7

US-09-878-603-73
Sequence 73, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czeizmak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 73
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-73

Query Match
Best Local Similarity 96.5%; Score 110; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 1 CCYDGASVNNDETCEORAR 20

RESULT 8

US-09-878-603-54
Sequence 54, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czeizmak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-54

Query Match
Best Local Similarity 95.6%; Score 109; DB 9; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAA 19
DB 1 CCYDGASVNNDETCEORAA 19

RESULT 9

US-09-878-603-64
Sequence 64, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czeizmak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-64

Query Match
Best Local Similarity 94.7%; Score 108; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 1 CCYDGASVNNDETCEORAR 20

RESULT 10

US-09-878-603-65
Sequence 65, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czeizmak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 65
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-65

Query Match
Best Local Similarity 94.7%; Score 108; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20

Db 1 CCYDGASVNNDETCEORAR 20

RESULT 11
US-09-878-603-72

; Sequence 72, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; PRIOR FILING DATE: 2001-06-11
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 72
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-72

Query Match 93.0%; Score 106; DB 9; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.5e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
Db 1 CCYDGASVNNDETCEORAR 20

RESULT 12
US-09-878-603-55

; Sequence 55, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; PRIOR FILING DATE: 2001-06-11
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-55

Query Match 92.1%; Score 105; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORA 18
Db 1 CCYDGASVNNDETCEORA 18

RESULT 13

US-09-878-603-59
; Sequence 59, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; PRIOR FILING DATE: 2001-06-11
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 59
; LENGTH: 19
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-59

Query Match 92.1%; Score 105; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCYDGASVNNDETCEORAR 20
Db 1 CCYDGASVNNDETCEORAR 19

RESULT 14
US-09-878-603-66

; Sequence 66, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; PRIOR FILING DATE: 2001-06-11
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 66
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-66

Query Match 89.5%; Score 102; DB 9; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
Db 1 CCYDGASVNNDETCEORAR 20

RESULT 15
US-09-878-603-56
; Sequence 56, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.

Sun May 4 10:03:41 2003

us-09-651-685a-5.closed.rabb

Page 5

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? APPLICANT: Huber-Lang, Markus
? APPLICANT: Sarma, Vidya
? APPLICANT: Czermak, Boris
? TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
? FILE REFERENCE: UM-03783
? CURRENT APPLICATION NUMBER: US/09/878,603
? CURRENT FILING DATE: 2001-06-11
? PRIOR APPLICATION NUMBER: 09/387,671
? PRIOR FILING DATE: 1999-08-31
? NUMBER OF SEQ ID NOS: 74
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO: 56
? LENGTH: 17
? TYPE: PRT
? ORGANSIM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-56

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Best Local Similarity	100.0%	Pred 10:	1.6e-08:	
Matches	17:	Conservative	0:	Mismatches 0:
				Indels 0:
				Gaps 0:

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Db      1 CCYDGASVNNDETCEQR 17
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Search completed: May 1, 2003, 22:35:14
Job time : 45 secs

Page 5

1-2

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:24:53 ; Search time 29 Seconds
(without alignments)
20.292 Million cell updates/sec

Title: US-09-651-685A-5
Perfect score: 114
Sequence: 1 CCYDGSYNDPTEQRAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 132970

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	35	30.7	16	1	US-08-477-383-14
3	35	30.7	16	1	US-08-487-174-14
4	35	30.7	16	1	US-08-480-750-14
5	35	30.7	16	1	US-09-441-502B-31
6	34.5	30.3	18	1	US-08-137-800-32
7	34.5	30.3	18	1	US-08-477-383-32
8	34.5	30.3	18	1	US-08-487-174-32
9	34.5	30.3	18	1	US-08-480-750-32
10	34	29.8	15	4	US-08-975-040-3
11	34	29.8	19	1	US-08-392-646-18
12	34	29.8	19	4	US-08-975-040-2
13	34	29.8	19	4	US-08-975-040-19
14	34	29.8	19	4	US-09-101-927-17
15	34	29.8	19	4	US-09-101-927-19
16	34	29.8	19	4	US-09-441-502B-30
17	32	28.1	18	1	US-08-159-340A-32
18	31	27.2	16	1	US-08-574-763-3
19	31	27.2	20	5	PCT-US95-06726-19
20	30	26.3	11	3	US-08-838-413A-14
21	29.5	25.9	18	1	US-08-137-800-13
22	29.5	25.9	18	1	US-08-137-800-31
23	29.5	25.9	18	1	US-08-477-383-13
24	29.5	25.9	18	1	US-08-477-383-31
25	29.5	25.9	18	1	US-08-487-174-13
26	29.5	25.9	18	1	US-08-487-174-31
27	29.5	25.9	18	1	US-08-480-750-13

28	29.5	25.9	18	1	US-08-480-750-31	Sequence 31, Appl
29	29	25.4	10	1	US-08-421-702A-79	Sequence 79, Appl
30	29	25.4	10	1	US-08-303-052A-32	Sequence 32, Appl
31	29	25.4	10	1	US-08-421-696A-79	Sequence 79, Appl
32	29	25.4	10	1	US-08-421-697A-79	Sequence 79, Appl
33	29	25.4	10	1	US-08-421-698A-79	Sequence 79, Appl
34	29	25.4	10	2	US-08-421-695A-32	Sequence 32, Appl
35	29	25.4	10	3	US-08-461-384B-9	Sequence 9, Appl
36	29	25.4	10	3	US-08-407-207A-6	Sequence 6, Appl
37	29	25.4	13	4	US-09-136-769A-7	Sequence 7, Appl
38	29	25.4	13	4	US-09-136-769A-18	Sequence 18, Appl
39	29	25.4	13	4	US-08-335-303-20	Sequence 20, Appl
40	29	25.4	19	1	US-08-290-448A-49	Sequence 49, Appl
41	29	25.4	19	1	US-08-290-448A-49	Sequence 49, Appl
42	29	25.4	19	1	US-08-175-069A-49	Sequence 49, Appl
43	29	25.4	19	4	US-08-461-939B-49	Sequence 49, Appl
44	29	25.4	19	4	US-08-464-000-49	Sequence 49, Appl
45	29	25.4	19	4	US-08-464-000-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-137-800-14
; Sequence 14, Application US/08137800
; Patent No. 5514774
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hilliard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Santos, Ameurflina D.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137, 800
; FILING DATE: 19-OCT-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-104763
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-4810
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus bandanus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6..14
; OTHER INFORMATION: /note= "Xaa(6) is Pro or
; OTHER INFORMATION: Hydroxy-Pro, Xaa(13) is Pro or Hydroxy-Pro;
; OTHER INFORMATION: Xaa(14) is Asp or beta-carboxyaspartate"

US-08-137-800-14

Query Match

Best Local Similarity 42.9%; Score 35; DB 1; Length 16;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;QY 1 CCYDGASVNDCTC 14
1 : 1111 1
Db 3 CSHXACSVNNXXIC 16

RESULT 2

US-08-477-383-14
; Sequence 14, Application US/08477383
; Patent No. 5589340
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurflino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,383
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus bandanus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6..14
; OTHER INFORMATION: /note= "Xaa(6) is Pro or
; OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro; Xaa(14) is Asp or
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."

US-08-477-383-14

Query Match

Best Local Similarity 42.9%; Score 35; DB 1; Length 16;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;QY 1 CCYDGASVNDCTC 14
1 : 1111 1
Db 3 CSHXACSVNNXXIC 16

RESULT 3

US-08-487-174-14
; Sequence 14, Application US/08487174
; Patent No. 5595972
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurflino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,174
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus bandanus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6..14
; OTHER INFORMATION: /note= "Xaa(6) is Pro or
; OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro; Xaa(14) is Asp
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."

US-08-487-174-14

Query Match 30.7%; Score 35; DB 1; Length 16;
Best Local Similarity 42.9%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETC 14
| : |||| |
DB 3 CSHXACSVNXXIC 16

RESULT 4

US-08-480-750-14
; Sequence 14, Application US/08480750
; Patent No. 5633347
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurflino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,750
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus bandanus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6..14
; OTHER INFORMATION: /note= "Xaa(6) is Pro or
; OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro; Xaa(14) is Asp or
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."

US-08-480-750-14

Query Match 30.7%; Score 35; DB 1; Length 16;
Best Local Similarity 42.9%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETC 14
| : |||| |
DB 3 CSHXACSVNXXIC 16

RESULT 5

US-09-441-502B-31
; Sequence 31, Application US/09441502B
; Patent No. 6455041
; GENERAL INFORMATION:
; APPLICANT: Dundar, Bonita S.
; TITLE OF INVENTION: IMMUNOGENIC EPITOPES OF THE HUMAN ZONA PELLUCIDA PROTEIN
; FILE REFERENCE: 12231.20501
; CURRENT APPLICATION NUMBER: US/09/441,502B
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-502B-31

Query Match 30.7%; Score 35; DB 4; Length 19;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCYDGASVNN 10
| | | | |
DB 5 CCYSSEEVNS 14

RESULT 6

US-08-137-800-32
; Sequence 32, Application US/08137800
; Patent No. 5514774
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurflino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,800
; FILING DATE: 19-OCT-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-104763
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3..4
OTHER INFORMATION: /note="Xaa is Pro or Hydroxy-Pro"
US-08-137-800-32

Query Match 30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY 1 CCYDGA-SVNDETC 14
||:|:||||:|
Db 4 CCSNPACVNNPQIC 18

RESULT 7
US-08-477-383-32
Sequence 32, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurifino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORGANISM: Conus ermineus

ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note="Xaa is Pro or Hydroxy-Pro."
US-08-477-383-32

Query Match 30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY 1 CCYDGA-SVNDETC 14
||:|:||||:|
Db 4 CCSNPACVNNPQIC 18

RESULT 8
US-08-487-174-32
Sequence 32, Application US/08487174
Patent No. 5593972
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurifino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus

FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note="Xaa is Pro or Hydroxy-Pro."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: /note="The C-terminus is
OTHER INFORMATION: preferably amidated."
US-08-487-174-32

Query Match 30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 CCYDGA-SVNDTC 14
DB 4 CCSNPACVNNPQIC 18

RESULT 9
US-08-480-750-32
Sequence 32, Application US/08480750
Patent No. 5633347
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hilliard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Amelino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site

LOCATION: 3
OTHER INFORMATION: /note="Xaa is Pro or Hydroxy-Pro."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: /note="The C-terminus is
OTHER INFORMATION: preferably amidated."
US-08-480-750-32

Query Match 30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 CCYDGA-SVNDTC 14
DB 4 CCSNPACVNNPQIC 18

RESULT 10
US-08-975-040-3
Sequence 3, Application US/08975040
Patent No. 6251620
GENERAL INFORMATION:
APPLICANT: HATADA, MARCOS
APPLICANT: LU, XIODE
APPLICANT: LAIRD, ELLEN
APPLICANT: KARAS, JENNIFER
APPLICANT: ZOLLER, MARK
APPLICANT: HOLT, DENNIS
TITLE OF INVENTION: MACHINE READABLE STORAGE MEDIUM RELATING
TITLE OF INVENTION: TO ZAP-FAMILY PROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID L. BERSTEIN, ARIAD PHARMACEUTICALS,
STREET: 26 LANDSDOWNE STREET
CITY: CAMBRIDGE
STATE: MA
COUNTRY: US
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,040
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/605,578
FILING DATE: 22-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, DAVID L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 347F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-1828
TELEFAX: 617-494-1828
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product="phosphotyrosine"
OTHER INFORMATION: /label="pTyr"
OTHER INFORMATION: /note="phosphorylated tyrosine"

NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: /product= "phosphotyrosine"
OTHER INFORMATION: /label= ptyr
OTHER INFORMATION: /note= "phosphorylated tyrosine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "Acetylated"
OTHER INFORMATION: /label= Ac
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: /product= "amidated"
OTHER INFORMATION: /label= NH2
US-08-975-040-3

Query Match 29.8%; Score 34; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 YDGASVNDCTE 15
DB 1 YTGSLSTRNOETYE 13

RESULT 11
US-08-392-646-18
Sequence 18, Application US/08392646
Patent No. 5710129
GENERAL INFORMATION:
APPLICANT: LYNCH, Berkley A.
APPLICANT: WEIGLE, Manfred
TITLE OF INVENTION: NEW INHIBITORS OF SH2-MEDIATED PROCESSES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Pharmaceuticals, Inc.
STREET: 26 Landsdowne Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139-4234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,646
FILING DATE: 23-FEB-1995
CLASSIFICATION: 560
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, David L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-0400
TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "phosphotyrosine"
OTHER INFORMATION: /label= YPO4
OTHER INFORMATION: /note= "phosphorylated tyrosine"

NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: /product= "phosphotyrosine"
OTHER INFORMATION: /label= YPO4
OTHER INFORMATION: /note= "phosphorylated tyrosine"
US-08-392-646-18

Query Match 29.8%; Score 34; DB 1; Length 19;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 YDGASVNDCTE 15
DB 4 YTGSLSTRNOETYE 16

RESULT 12
US-08-975-040-2
Sequence 2, Application US/08975040
Patent No. 6251620
GENERAL INFORMATION:
APPLICANT: HATADA, MARCOS
APPLICANT: LU, XIADDE
APPLICANT: LAIRD, ELLEN
APPLICANT: KARAS, JENNIFER
APPLICANT: ZOLLER, MARK
TITLE OF INVENTION: MACHINE READABLE STORAGE MEDIUM RELATING
TO ZAP-FAMILY PROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID L. BERSTEIN, ARIAD PHARMACEUTICALS,
INC.
STREET: 26 LANDSDOWNE STREET
CITY: CAMBRIDGE
STATE: MA
COUNTRY: US
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,040
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/605,578
FILING DATE: 22-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, DAVID L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 347F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-1828
TELEFAX: 617-494-0400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "phosphotyrosine"
OTHER INFORMATION: /label= ptyr
OTHER INFORMATION: /note= "phosphorylated tyrosine"
NAME/KEY: Modified-site
LOCATION: 15

OTHER INFORMATION: /product= "phosphotyrosine"
OTHER INFORMATION: /label= ptyr
OTHER INFORMATION: /note= "phosphorylated tyrosine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "acetylated"
OTHER INFORMATION: /label= Ac
FEATURE:
NAME/KEY: Modified-site
LOCATION: 19
OTHER INFORMATION: /product= "amidated"
OTHER INFORMATION: /label= NH2
US-08-975-040-2

Query Match 29.8%; Score 34; DB 4; Length 19;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 YDGASVNDCE 15
DB 4 YTGSTRNOEY 16

RESULT 13
US-08-975-040-19
Sequence 19, Application US/08975040
Patent No. 6251620
GENERAL INFORMATION:
APPLICANT: HATADA, MARCOS
APPLICANT: LU, XIODE
APPLICANT: LAIRD, ELLEN
APPLICANT: KARAS, JENNIFER
APPLICANT: ZOLLER, MARK
APPLICANT: HOLT, DENNIS
TITLE OF INVENTION: MACHINE READABLE STORAGE MEDIUM RELATING
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID L. BERSTEIN, ARIAD PHARMACEUTICALS,
STREET: 26 LANDSDOWNE STREET
CITY: CAMBRIDGE
STATE: MA
COUNTRY: US
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975.040
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/605.578
FILING DATE: 22-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, DAVID L.
REGISTRATION NUMBER: 31,235
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-0400
TELEFAX: 617-494-1828
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "phosphotyrosine"
OTHER INFORMATION: /label= YPO4
OTHER INFORMATION: /note= "phosphorylated tyrosine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: /product= "phosphotyrosine"
OTHER INFORMATION: /label= YPO4
OTHER INFORMATION: /note= "phosphorylated tyrosine"
US-08-975-040-19

Query Match 29.8%; Score 34; DB 4; Length 19;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 YDGASVNDCE 15
DB 4 YTGSTRNOEY 16

RESULT 14
US-09-101-927-17
Sequence 17, Application US/09101927
Patent No. 6303319
GENERAL INFORMATION:
APPLICANT: Rickles, Richard J
TITLE OF INVENTION: Cell-Based Assay
FILE REFERENCE: 336A PCT/US
CURRENT APPLICATION NUMBER: US/09/101.927
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: PCT/US97/026735
EARLIER FILING DATE: 1997-02-21
EARLIER APPLICATION NUMBER: 60/012,218
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 17
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)
OTHER INFORMATION: PHOSPHORYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (15)
OTHER INFORMATION: PHOSPHORYLATION
US-09-101-927-17

Query Match 29.8%; Score 34; DB 4; Length 19;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 YDGASVNDCE 15
DB 4 YTGSTRNOEY 16

RESULT 15
US-09-101-927-19
Sequence 19, Application US/09101927
Patent No. 6303319
GENERAL INFORMATION:
APPLICANT: Rickles, Richard J
TITLE OF INVENTION: Cell-Based Assay
FILE REFERENCE: 336A PCT/US
CURRENT APPLICATION NUMBER: US/09/101.927
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: PCT/US97/026735

; EARLIER FILING DATE: 1997-02-21
; EARLIER APPLICATION NUMBER: 60/012,218
; EARLIER FILING DATE: 1996-02-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: PHOSPHORYLATION
US-09-101-927-19

Query Match 29.8%; Score 34; DB 4; Length 19;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 YDGASVNDNDECE 15
| | | | | | |
Db 4 YTGILSTRNOETIVE 16

Search completed: May 1, 2003, 22:28:15
Job time : 30 secs